

GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2003, 01:06:09 ; Search time 1066 seconds  
(without alignments)  
9784.140 Million cell updates/sec

Title: US-10-037-591a-1

Perfect score: 644

Sequence: 1 ctcaagtcactcctctaaataa.....ggcccggtgtgagcgtag 644

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Capext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estnu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_estli:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_man:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID       | Description        |
|------------|-------|-------------|--------|-------------|--------------------|
| 1          | 296.4 | 46.0        | 524    | 9 AI430337  | AI430337 mf68b10.y |
| 2          | 249.6 | 38.8        | 420    | 14 W88186   | W88186 mf68b10.r1  |
| 3          | 229   | 35.6        | 553    | 13 BM540145 | BM540145 hb18f07.g |
| 4          | 145.4 | 22.6        | 344    | 12 BG609875 | BG609875 324181.MA |
| 5          | 96.6  | 15.0        | 480    | 13 BM124559 | BM124559 L0541G02- |
| 6          | 96.6  | 15.0        | 549    | 14 BQ554452 | BQ554452 H4028C03- |

|      |      |     |      |    |          |                    |
|------|------|-----|------|----|----------|--------------------|
| C 7  | 47.4 | 7.4 | 925  | 17 | CNS0091P | AL053013 Drosophil |
| C 8  | 47   | 7.3 | 997  | 17 | CNS006DN | AL065132 Drosophil |
| C 9  | 43.8 | 6.8 | 868  | 12 | BG821981 | BG821981 602726077 |
| C 10 | 43.2 | 6.7 | 925  | 17 | CNS0091P | AL053013 Drosophil |
| C 11 | 43   | 6.6 | 568  | 14 | BQ574994 | BQ574994 UT-H-E21- |
| C 12 | 42.8 | 6.6 | 440  | 14 | BQ779177 | BQ779177 946117E05 |
| C 13 | 42.4 | 6.6 | 839  | 17 | CNS004NB | AL054280 Drosophil |
| C 14 | 42.2 | 6.6 | 460  | 10 | BE357122 | BE357122 DGL-146.B |
| C 15 | 42.2 | 6.6 | 486  | 9  | AI388531 | AI388531 GH19472.5 |
| C 16 | 42.2 | 6.6 | 586  | 10 | BE357121 | BE357121 DGL-146.B |
| C 17 | 42.2 | 6.6 | 588  | 13 | BM055698 | BM055698 id85H04.x |
| C 18 | 42.2 | 6.6 | 633  | 13 | BM330143 | BM330143 PIC1.47.F |
| C 19 | 42.2 | 6.6 | 652  | 10 | BE362682 | BE362682 DGL-88.H0 |
| C 20 | 41.6 | 6.5 | 441  | 9  | AI064196 | AI064196 GH04480.5 |
| C 21 | 41.4 | 6.4 | 373  | 9  | AI867949 | AI867949 W900B08.x |
| C 22 | 41.4 | 6.4 | 396  | 9  | AA680405 | AA680405 Z138H02.S |
| C 23 | 41.4 | 6.4 | 405  | 9  | AI375735 | AI375735 ta64C02.X |
| C 24 | 41.4 | 6.4 | 590  | 12 | BF510968 | BF510968 UT-H-B14- |
| C 25 | 41.4 | 6.4 | 629  | 14 | BM826445 | BM826445 K-EST0098 |
| C 26 | 41.2 | 6.4 | 463  | 13 | BM381881 | BM381881 MEST541-D |
| C 27 | 41.2 | 6.4 | 488  | 9  | AI854942 | AI854942 605094E01 |
| C 28 | 41.2 | 6.4 | 527  | 10 | AW787570 | AW787570 945011B07 |
| C 29 | 41.2 | 6.4 | 540  | 10 | AW927918 | AW927918 945011B07 |
| C 30 | 41.2 | 6.4 | 556  | 10 | AW787571 | AW787571 945011B07 |
| C 31 | 41.2 | 6.4 | 567  | 10 | BE129743 | BE129743 946003H07 |
| C 32 | 41.2 | 6.4 | 567  | 14 | BQ280219 | BQ280219 1091036B1 |
| C 33 | 41.2 | 6.4 | 583  | 9  | AI833725 | AI833725 605094E01 |
| C 34 | 41.2 | 6.4 | 584  | 14 | BQ279494 | BQ279494 1091036B1 |
| C 35 | 41.2 | 6.4 | 586  | 10 | BE511474 | BE511474 946061B04 |
| C 36 | 41.2 | 6.4 | 609  | 13 | BM381419 | BM381419 MEST534-E |
| C 37 | 41.2 | 6.4 | 615  | 10 | AW424676 | AW424676 707058E02 |
| C 38 | 41   | 6.4 | 483  | 9  | AI388053 | AI388053 GH18791.5 |
| C 39 | 40.8 | 6.3 | 1063 | 17 | CNS07A2Y | AL436064 T3 end of |
| C 40 | 40.6 | 6.3 | 425  | 13 | BI396114 | BI396114 949044E02 |
| C 41 | 40.6 | 6.3 | 441  | 13 | BM382130 | BM382130 MEST545-A |
| C 42 | 40.6 | 6.3 | 468  | 12 | BF150243 | BF150243 uy83e02.Y |
| C 43 | 40.6 | 6.3 | 497  | 13 | BI388823 | BI388823 949046B01 |
| C 44 | 40.6 | 6.3 | 553  | 9  | AI323984 | AI323984 mb22a01.x |
| C 45 | 40.6 | 6.3 | 602  | 13 | BM053185 | BM053185 id66606.x |

## ALIGNMENTS

RESULT 1  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AI430337  
mf68b10.y1 Soares mouse embryo NDME13.5 14.5 Mus musculus CDNA  
Clone IMAGE:419419 5', mRNA linear EST 15-MAR-2000  
AI430337  
AI430337.1 GI:4276173  
EST.  
house mouse.  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 524)  
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person  
B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter  
E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  
Waterston,R. and Wilson,R.  
The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)  
Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
This read is a RESEQUENCE of a previously sequenced mouse clone

This read has been verified (found to hit its original self in the correct orientation)

Correct Orientation/  
MGI:253971  
Seq primer: -40RP from Gibco  
High quality sequence stop: 476  
POLYA=NO.

| FEATURES                | SOURCE     |
|-------------------------|------------|
| 1. <b>Feature 1</b>     | Source 1   |
| 2. <b>Feature 2</b>     | Source 2   |
| 3. <b>Feature 3</b>     | Source 3   |
| 4. <b>Feature 4</b>     | Source 4   |
| 5. <b>Feature 5</b>     | Source 5   |
| 6. <b>Feature 6</b>     | Source 6   |
| 7. <b>Feature 7</b>     | Source 7   |
| 8. <b>Feature 8</b>     | Source 8   |
| 9. <b>Feature 9</b>     | Source 9   |
| 10. <b>Feature 10</b>   | Source 10  |
| 11. <b>Feature 11</b>   | Source 11  |
| 12. <b>Feature 12</b>   | Source 12  |
| 13. <b>Feature 13</b>   | Source 13  |
| 14. <b>Feature 14</b>   | Source 14  |
| 15. <b>Feature 15</b>   | Source 15  |
| 16. <b>Feature 16</b>   | Source 16  |
| 17. <b>Feature 17</b>   | Source 17  |
| 18. <b>Feature 18</b>   | Source 18  |
| 19. <b>Feature 19</b>   | Source 19  |
| 20. <b>Feature 20</b>   | Source 20  |
| 21. <b>Feature 21</b>   | Source 21  |
| 22. <b>Feature 22</b>   | Source 22  |
| 23. <b>Feature 23</b>   | Source 23  |
| 24. <b>Feature 24</b>   | Source 24  |
| 25. <b>Feature 25</b>   | Source 25  |
| 26. <b>Feature 26</b>   | Source 26  |
| 27. <b>Feature 27</b>   | Source 27  |
| 28. <b>Feature 28</b>   | Source 28  |
| 29. <b>Feature 29</b>   | Source 29  |
| 30. <b>Feature 30</b>   | Source 30  |
| 31. <b>Feature 31</b>   | Source 31  |
| 32. <b>Feature 32</b>   | Source 32  |
| 33. <b>Feature 33</b>   | Source 33  |
| 34. <b>Feature 34</b>   | Source 34  |
| 35. <b>Feature 35</b>   | Source 35  |
| 36. <b>Feature 36</b>   | Source 36  |
| 37. <b>Feature 37</b>   | Source 37  |
| 38. <b>Feature 38</b>   | Source 38  |
| 39. <b>Feature 39</b>   | Source 39  |
| 40. <b>Feature 40</b>   | Source 40  |
| 41. <b>Feature 41</b>   | Source 41  |
| 42. <b>Feature 42</b>   | Source 42  |
| 43. <b>Feature 43</b>   | Source 43  |
| 44. <b>Feature 44</b>   | Source 44  |
| 45. <b>Feature 45</b>   | Source 45  |
| 46. <b>Feature 46</b>   | Source 46  |
| 47. <b>Feature 47</b>   | Source 47  |
| 48. <b>Feature 48</b>   | Source 48  |
| 49. <b>Feature 49</b>   | Source 49  |
| 50. <b>Feature 50</b>   | Source 50  |
| 51. <b>Feature 51</b>   | Source 51  |
| 52. <b>Feature 52</b>   | Source 52  |
| 53. <b>Feature 53</b>   | Source 53  |
| 54. <b>Feature 54</b>   | Source 54  |
| 55. <b>Feature 55</b>   | Source 55  |
| 56. <b>Feature 56</b>   | Source 56  |
| 57. <b>Feature 57</b>   | Source 57  |
| 58. <b>Feature 58</b>   | Source 58  |
| 59. <b>Feature 59</b>   | Source 59  |
| 60. <b>Feature 60</b>   | Source 60  |
| 61. <b>Feature 61</b>   | Source 61  |
| 62. <b>Feature 62</b>   | Source 62  |
| 63. <b>Feature 63</b>   | Source 63  |
| 64. <b>Feature 64</b>   | Source 64  |
| 65. <b>Feature 65</b>   | Source 65  |
| 66. <b>Feature 66</b>   | Source 66  |
| 67. <b>Feature 67</b>   | Source 67  |
| 68. <b>Feature 68</b>   | Source 68  |
| 69. <b>Feature 69</b>   | Source 69  |
| 70. <b>Feature 70</b>   | Source 70  |
| 71. <b>Feature 71</b>   | Source 71  |
| 72. <b>Feature 72</b>   | Source 72  |
| 73. <b>Feature 73</b>   | Source 73  |
| 74. <b>Feature 74</b>   | Source 74  |
| 75. <b>Feature 75</b>   | Source 75  |
| 76. <b>Feature 76</b>   | Source 76  |
| 77. <b>Feature 77</b>   | Source 77  |
| 78. <b>Feature 78</b>   | Source 78  |
| 79. <b>Feature 79</b>   | Source 79  |
| 80. <b>Feature 80</b>   | Source 80  |
| 81. <b>Feature 81</b>   | Source 81  |
| 82. <b>Feature 82</b>   | Source 82  |
| 83. <b>Feature 83</b>   | Source 83  |
| 84. <b>Feature 84</b>   | Source 84  |
| 85. <b>Feature 85</b>   | Source 85  |
| 86. <b>Feature 86</b>   | Source 86  |
| 87. <b>Feature 87</b>   | Source 87  |
| 88. <b>Feature 88</b>   | Source 88  |
| 89. <b>Feature 89</b>   | Source 89  |
| 90. <b>Feature 90</b>   | Source 90  |
| 91. <b>Feature 91</b>   | Source 91  |
| 92. <b>Feature 92</b>   | Source 92  |
| 93. <b>Feature 93</b>   | Source 93  |
| 94. <b>Feature 94</b>   | Source 94  |
| 95. <b>Feature 95</b>   | Source 95  |
| 96. <b>Feature 96</b>   | Source 96  |
| 97. <b>Feature 97</b>   | Source 97  |
| 98. <b>Feature 98</b>   | Source 98  |
| 99. <b>Feature 99</b>   | Source 99  |
| 100. <b>Feature 100</b> | Source 100 |

```

location/Vvairillets
1..524
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:419419"
/clone_lib="Soares mouse"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc"
/lab_host="Dhi08"
/notes="Vector: pT73D-Pa
polylinker; site_1: Not
I was primed with a Not I
TGTTACCAATCTCAAGTGGGAGCG
T 3'), on equal amounts
14.5dpc embryos [total R
State Univ., from 2 ]; d
Eco RI adaptors (Pharmac
cloned into the Not I an
pT73 vector. Library we
normalization, and was c
M.Fatima Bonaldo. "
100 a 177 c 150 g
BASE COUNT

```

| BASE COUNT | 100 a | 177 c | 150 g | 97 t |
|------------|-------|-------|-------|------|
| ORIGIN     |       |       |       |      |

Query Match 46.0%; Score 296.4; DB 9; Length 524;  
Best Local Similarity 84.5%; Pred. NO. 6.2e-61;  
Matches 333; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

|     |    |                                                                  |     |
|-----|----|------------------------------------------------------------------|-----|
| 251 | Qy | CTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCGCTGTGCCTCCCTCTAGAGCCCTGTCTAGGCC | 310 |
| 11  | Db | CCGGAGGAGTGGCTGAAAGTGGAGCTCTCATGCTGTGTCTCCGCCAGAGCCCTCTGAGCCA    | 70  |
| 311 | Qy | CAACGCCACCCAGAGTCTGTGAGGCCAGTGAAGATGACCCCTCTCAACAGCAGAGGCCAT     | 370 |
| 71  | Db | CACCCACCGCAGAACTCTGCGAGGCCAGCTAGGATGGCCCCCTCAACAGCAGGCCAT        | 130 |
| 371 | Qy | CTCCCCCTGGAGATATGAGTTGGACAGAGACTTTGAACCGGCTCCCCCAGGACCTGTACCA    | 430 |
| 131 | Db | CTCTCTTTGGAGCTATGAGTTGGACAGGACTTTGAATCGGTCGCCCCAGGACCTGTACCA     | 190 |
| 431 | Qy | CGCCCGTTGGCTGTGCGCGGACACTGCGCTAGCCTTACAGACAGGCTGCCACATGGACCCCG   | 490 |
| 191 | Db | CGCTCGATGCTGTGGCCACACTTGCCTAGCCCTTACAGACAGGCTCCACATGGAGCCCGT     | 250 |
| 491 | Qy | GGCCACTCGGAGCTGCTTACCACAAACAGACTGCTTCTACCGGCGGCCATGCCATGG        | 550 |
| 251 | Db | GGGCACTCCGTCGCCCTTTACCACAAACAGAGCGTCTTCTACCGGCGGCCATGCCATGG      | 310 |
| 551 | Qy | CGAGAGGGGACCCACAAAGGGCTACTGCGCTGGAGCGCAGGCTGTACCGTGTTCCTTTAGC    | 610 |
| 311 | Db | CGAGGAGGTACCATCGCCGCTACTGCTTGGAGCGCAGGCTTACCGGAGTCTCCTTGGC       | 370 |
| 611 | Qy | TTGTGTGTGTGGGCCCCCGTGTGATGGGCTAG                                 | 644 |
| 371 | Db | TTGTGTGTGTGGGCCCCCGGCTTATGGCTTAG                                 | 404 |

## RESULT 2

|            |                                       |                     |         |                   |                 |
|------------|---------------------------------------|---------------------|---------|-------------------|-----------------|
| W88186     | W88186                                | 420 bp              | mrna    | linear            | EST 12-SEP-1996 |
| LOCUS      | mf68b10.r1                            | Soares mouse embryo | NBM13.5 | 14.5 Mus musculus | CDNA            |
| DEFINITION | clone IMAGE:419419 5', mRNA sequence. |                     |         |                   |                 |
| ACCESSION  | W88186                                |                     |         |                   |                 |
| VERSION    | W88186.1                              | GI:1542472          |         |                   |                 |
| KEYWORDS   | EST.                                  |                     |         |                   |                 |

SOURCE ORGANISM

REFERENCE  
AUTHORS

| TITLE                                                     | JOURNAL                           | COMMENT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|-----------------------------------------------------------|-----------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1. The Role of the Teacher in the 21st Century            | Journal of Educational Research   | 1. The author argues that the teacher's role is becoming increasingly complex and multifaceted in the 21st century. This is due to the rapid pace of technological change and the increasing diversity of the student population. The teacher must now be a facilitator of learning, rather than a sole source of knowledge. This requires a shift in the teacher's mindset and a focus on developing students' critical thinking and problem-solving skills. The author also discusses the importance of collaboration and communication in the classroom, and the need for ongoing professional development for teachers. |
| 2. The Impact of Social Media on Education                | Journal of Educational Technology | 2. The author explores the impact of social media on education, both in terms of learning and teaching. On the one hand, social media can provide a wealth of resources and opportunities for students to learn and collaborate. It can also be a source of distraction and a barrier to learning. The author discusses the challenges of integrating social media into the classroom and the need for teachers to be aware of the potential risks and benefits. The author also suggests some strategies for using social media effectively in the classroom, such as using it for research and collaboration.             |
| 3. The Future of Education: A Vision for the 21st Century | Journal of Educational Leadership | 3. The author presents a vision for the future of education, one that is centered on the needs of the individual student. This vision is based on the principles of personalized learning, which allows students to learn at their own pace and in their own way. The author also discusses the importance of data-driven decision making in education, and the need for schools to be more transparent and accountable. The author concludes by stating that the future of education is bright, but it will only be realized if we are willing to embrace change and innovation.                                           |

Unpublished (1996)  
On Sep 12, 1996 this sequence version replaced gi:1402263.  
Contact: Marra M/Mouse EST Project  
WashU-HMMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact  
IMAGE Consortium (info@image.llnl.gov) for further information  
MGI:253971  
Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 408.

FEATURES  
SOURCE

```

1. .420
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:419419"
/clone_lib="Soares mouse embryo NBMEL3.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/notes="vector: pT7T3D-Pac (Pharmacia) with a m
polylinker; site 1: Not I; Site 2: Eco RI; 1st
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAACTGATGGGGAGCGCGCGGAAATTTTCTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc
14.5dpc embryos [total RNA provided by Minoru
State Univ., from 2 1; double-stranded cDNA was
Eco RI adaptors (Pharmacia), digested with Not
cloned into the Not I and Eco RI sites of the
pT73 vector. Library went through one round of
normalization, and was constructed by Bento So
M.Fatima Bonaldo."

```

[illegible]

| Query Match           | 38.8%                                                        | Score 249.6                                                 | DB 14         | Length 420 |        |
|-----------------------|--------------------------------------------------------------|-------------------------------------------------------------|---------------|------------|--------|
| Best Local Similarity | 80.1%                                                        | Prod. No. 1.le-49                                           |               |            |        |
| Matches 330           | Conservative                                                 | 0                                                           | Mismatches 79 | Indels 3   | Gaps 3 |
| 233                   | CAGCAAAGGCGAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCC | 292                                                         |               |            |        |
| y                     |                                                              |                                                             |               |            |        |
| b                     | 3                                                            | CGGACAGGCGGCACAAACCCGGAGAGTGCTGAAGTGGAGCTCTGCATCTGTATCCCC   | 62            |            |        |
| 293                   | CCTAGAGCCTGTAGGCCOAAACCGCCACCCAGAGTCTGTAGGCGCAGTGAAGATGGACC  | 352                                                         |               |            |        |
| y                     |                                                              |                                                             |               |            |        |
| b                     | 63                                                           | CCGAGAGCCTGTAGGCCACACCCACGACAGAAATCCTCGAGGGCCAGCAAGGATGG-CC | 121           |            |        |
| 353                   | CCTCAACACAGGGCCATCTCCCTGGAGATATCAGTTGGACACAGACTTGAACCGCCT    | 412                                                         |               |            |        |
| y                     |                                                              |                                                             |               |            |        |
| b                     | 122                                                          | TCTCAACACAGGGGCCATCTCCTTTGGAGCTATCAGTTGGACAGGGACTTGAATCGGGT | 181           |            |        |
| 413                   | CCCCAAGGACCTGTACACGCCCGCTTGCTGTGCCCGCACTGCGTCAGCCTACACAGACGG | 472                                                         |               |            |        |
| y                     |                                                              |                                                             |               |            |        |
| b                     | 182                                                          | CCCCAAGGACTGGTACCACGCTCGATGCTGTGCCACACTGCGTCACGCTACACAGACGG | 241           |            |        |
| 473                   | CTCCCCACATGTGAACCCCGGGGCACTCGGAGCTGTCTTACCACACACAGACTGCTTCTA | 532                                                         |               |            |        |
| y                     |                                                              |                                                             |               |            |        |

|                           |                                                                      |                                                                  |                    |
|---------------------------|----------------------------------------------------------------------|------------------------------------------------------------------|--------------------|
| Qy                        | 186                                                                  | ATGCTATGGAACCCACAC-----CTACAGCCACTGGCCC                          | 221                |
| Db                        | 277                                                                  | ATGGCCATGGGAACCCACACCTCAATTTTGGGATCCGAAGGACTGCAACCCACTGGCCT      | 336                |
| Qy                        | 222                                                                  | AGCTGCTGCCCCAGCAAAAGGGAGGACACCTCTGAGAGACTGCTGAGGTGGAGCACTGTG     | 281                |
| Db                        | 337                                                                  | AACCTGCTGTCTCCAGCAAAAGGAGGAGGACCCCACTCATGAGTGGCTGAAGCGGACACTGTG  | 396                |
| Qy                        | 282                                                                  | CCTGTGCTCCTCCCTAGAGCCTGCTAGGCGCCAAACCGCCACCCAGACTCCTGTAGGCGCCAGT | 341                |
| Db                        | 397                                                                  | CTCAAGTTCCCGGAGAGACCACTAGCTCCTCACCCACACCCAGAATCTCTGCAAGCCAGT     | 456                |
| Qy                        | 342                                                                  | GAGATGGAGCCCTCTAACAGCAGGGGCCATCTCTCCCTCGAGATATGAGTTGGACAGAGAC    | 401                |
| Db                        | 457                                                                  | GAGAGCGGACCGCTCAACAGCAGGTCTATCTCTCCCTCGAAATATGAGTTGGACAGGAC      | 516                |
| Qy                        | 402                                                                  | TTGAACCGGCTCCCGCAGGACCTGTACCACGCCCGTT                            | 438                |
| Db                        | 517                                                                  | TTGAACCGGCTCCCGCAGGACCTGTACCACGCCCGTT                            | 553                |
| RESULT                    | 4                                                                    |                                                                  |                    |
| LOCUS                     | BG609875                                                             | 344 bp mRNA linear                                               | EST 17-APR         |
| DEFINITION                | 324181 MARC lPIG Sus scrofa cDNA 5', mRNA sequence.                  |                                                                  |                    |
| ACCESSION                 | BG609875                                                             |                                                                  |                    |
| VERSION                   | BG609875.1                                                           | GI:13659854                                                      |                    |
| KEYWORDS                  | EST.                                                                 |                                                                  |                    |
| SOURCE                    | pig.                                                                 |                                                                  |                    |
| ORGANISM                  | Sus scrofa                                                           |                                                                  |                    |
| REFERENCE                 | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;    |                                                                  |                    |
| AUTHORS                   | Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.             |                                                                  |                    |
|                           | Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas- |                                                                  |                    |
|                           | Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W. |                                                                  |                    |
|                           | and Keele, J.W.                                                      |                                                                  |                    |
| TITLE                     | Design and use of two pooled tissue normalized cDNA libraries for    |                                                                  |                    |
| JOURNAL                   | EST discovery in swine                                               |                                                                  |                    |
| COMMENT                   | Unpublished (2000)                                                   |                                                                  |                    |
|                           | Contact: Smith TPL                                                   |                                                                  |                    |
|                           | USDA, ARS, US Meat Animal Research Center                            |                                                                  |                    |
|                           | PO Box 166, Clay Center, NE 68933-0166, USA                          |                                                                  |                    |
|                           | Tel: 402 762 4366                                                    |                                                                  |                    |
|                           | Fax: 402 762 4390                                                    |                                                                  |                    |
|                           | Email: smith@email.marc.usda.gov                                     |                                                                  |                    |
|                           | Single pass sequencing. Bases called and alt_trimmed with phred      |                                                                  |                    |
|                           | v0.980904.e. Vector identified by cross_match with the 'minscore     |                                                                  |                    |
|                           | and -mismatch 12 options.                                            |                                                                  |                    |
| FEATURES                  | PCR Primers                                                          |                                                                  |                    |
| source                    | FORWARD: AGGAAACGCTATGACCAT                                          |                                                                  |                    |
|                           | BACKWARD: GTTTCCTCAGTCACGCG                                          |                                                                  |                    |
|                           | Plate: 100 row: G column: 12                                         |                                                                  |                    |
|                           | Seq primer: ATTTAGCTGACACTATAG.                                      |                                                                  |                    |
|                           | Location/Qualifiers                                                  |                                                                  |                    |
|                           | 1..344                                                               |                                                                  |                    |
|                           | /organism="Sus scrofa"                                               |                                                                  |                    |
|                           | /db_xref="taxon:9823"                                                |                                                                  |                    |
|                           | /clone_lib="MARC lPIG"                                               |                                                                  |                    |
|                           | /tissue_type="pooled"                                                |                                                                  |                    |
|                           | /lab_host="DH10B"                                                    |                                                                  |                    |
|                           | /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;              |                                                                  |                    |
|                           | Library made from pooled tissue from day 11, 13, 15, 2               |                                                                  |                    |
|                           | and 30 embryos."                                                     |                                                                  |                    |
| BASE COUNT                | 64 a 128 c 86 g 56 t                                                 |                                                                  |                    |
| ORIGIN                    |                                                                      |                                                                  |                    |
| Query Match               | 22.6%;                                                               | Score 145.4;                                                     | DB 12; Length 344; |
| Best Local Similarity     | 86.1%;                                                               | Pred. No. 1.2e-24;                                               |                    |
| Matches 161; Conservative | 0;                                                                   | Mismatches 26;                                                   | Indels 0; Gaps     |
| Qy                        | 389                                                                  | GTGTGACAGACTTGAACCGCTCCCCAGAGCACTGTACCAACGCCCGTTCGCTGTGCC        | 448                |
| Db                        | 158                                                                  | GTGTGACAGACTTGAACCGCTCCCCAGAGCACTGTACCAACGCCCGTTCGCTGTGCC        | 217                |

[illegible]

```

FEATURES
source
Location/Qualifiers
i. .480
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="niaEST:L0541G02-3"
/db_xref="taxon:10090"
/clone="L0541G02"
/clone_lib="NIA Mouse Newborn Heart cDNA Library"
/tissue_type="Newborn Heart"
/dev_stage="Newborn"
/lab_host="DH10B"
/note="Organ: Heart; Vector: pSPORT1 (Invitrogen); Site:1:
SalI; Site:2: NotI; Mouse cDNA project by the Laboratory
of Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
Double-stranded cDNAs were synthesized with an Oligo(dT)
primer [Invitrogen: 5'-
pGACTAGTCTAGATCGAGCGCCGCCCTTTTTTTTTTTT-3'] from
24.9 microgram of total RNA, treated with T4 DNA
polymerase, and purified by ethanol-precipitation. The
cDNAs were ligated to Lone-linker Lr-Sal3 (Ref.
Development 127:1737-1749 (2000) [PMID: 10725249]),
purified by phenol/chloroform, and separated from free
linkers by Centricon 100. Then, the cDNAs were digested
with SalI and NotI enzymes, and cloned into SalI and NotI
site of pSPORT1 plasmid vector. The DH10B E. coli host was
transformed with ligation mixture by the chemical method.
The average insert size is about 1.8 kb. The library was
constructed by Yulan Piao (NIA)."
```

|             |                                       |      |       |       |
|-------------|---------------------------------------|------|-------|-------|
| BASE COUNT  | 112 a                                 | 99 c | 143 g | 126 t |
| ORIGIN      |                                       |      |       |       |
| Query Match | 15.08; Score 96.6; DB 13; Length 480; |      |       |       |

|    | Best Local Similarity<br>Matches | 79.4%;<br>Conservative                                        | Pred: No. 6.6e-13;<br>0; | Mismatches<br>34; | Indels<br>2; | Gaps<br>2; |
|----|----------------------------------|---------------------------------------------------------------|--------------------------|-------------------|--------------|------------|
| Qy | 1                                | CTCAAGTCACCTCCCT-AAAAAGACAGCTGGAATAAATTTGAAATAACAAACACAGGCTTC | 59                       |                   |              |            |
| Db | 26                               | CTCAAGTCACCTCCCTCTAAAGAGTAGTGGAAATAAATTTGAAATAACAAACACAGGTTTC | 85                       |                   |              |            |
| Qy | 60                               | TGRAATAAATCAGGACTCCTAACCTGCTCCAGTCAGCTAGCTGCTCCACGAGGCGCTGTCA | 119                      |                   |              |            |
| Db | 86                               | TGRAATAAATCAGGACACTCAGCTGCTCCAGTCAGCCT-CTCTCAGAAGGCGCTGTCA    | 144                      |                   |              |            |
| Qy | 120                              | GTCAAGTCCCCACTTTGTGACTAGTGTGTCAGTGCCCGACAGCATGTACACAGTGGTTTG  | 174                      |                   |              |            |
| Db | 145                              | GGCAGGGGTAGTACCTGTGACTGTGTGAGCAGTGTCCGGCATGTACACAGTGCAGTG     | 199                      |                   |              |            |

|                                                                    |                                                                  |
|--------------------------------------------------------------------|------------------------------------------------------------------|
| RESULT                                                             | 6                                                                |
| BQ554452                                                           |                                                                  |
| LOCUS                                                              | H4028C03-3 NIA Mouse 7.4K cDNA Clone Set Mus musculus CDNA clone |
| DEFINITION                                                         | H4028C03 3', mRNA sequence.                                      |
| ACCESSION                                                          | BQ554452                                                         |
| VERSION                                                            | BQ554452.1 GI:21455340                                           |
| KEYWORDS                                                           | EST.                                                             |
| SOURCE                                                             | house mouse.                                                     |
| ORGANISM                                                           | Mus musculus                                                     |
| Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;           |                                                                  |
| Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |                                                                  |
| (bases 1 to 549)                                                   |                                                                  |
| VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., Martin  |                                                                  |
| ,P.R., Stagg,C.A., Bassey,U., Alba,K., Hamatani,T., Kargul,G.J.,   |                                                                  |
| Luo,A.G. and KO,M.S.H.                                             |                                                                  |
| Assembly, verification, and initial annotation of NIA 7.4K mouse   |                                                                  |
| Cdna clone set                                                     |                                                                  |
| Unpublished (2002)                                                 |                                                                  |
| Other ESTs: H4028C03-5                                             |                                                                  |
| TITLE                                                              |                                                                  |
| JOURNAL                                                            |                                                                  |
| COMMENT                                                            |                                                                  |

Contact: Yong Qian  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA  
Email: cdna@igsun.grc.nia.nih.gov  
This clone set has been freely distributed to the community. Please  
visit [http://igsun.grc.nia.nih.gov/cDNA/NIA\\_7\\_4k.html](http://igsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html) for details.  
Plate: H4028 row: C column: 03  
Seq primer: -21M13 Forward  
High quality sequence stop: 549  
POLYA=Yes.

```

FEATURES             Location/Qualifiers
     1..549
         /organism="Mus musculus"
         /strain="C57BL/6"
         /db_xref="niaEST:H4028C03-3"
         /db_xref="taxon:10090"
         /clone="H4028C03"
         /clone_lib="NIA Mouse 7.4K cDNA Clone Set"
         /sex="mixed"
         /dev_stage="mixed"
         /lab_host="DHI10B"
         /note="vector: pSPOR11; Site_1: SalI; Site_2: NotI; This
clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."
     129 a          121 c          164 g          135 t
BASE COUNT
ORIGIN

```

|    |                       |                                                                |                    |                |                   |
|----|-----------------------|----------------------------------------------------------------|--------------------|----------------|-------------------|
|    | Query Match           | 15.0%;                                                         | Score 96.6;        | DB 14;         | Length 549;       |
|    | Best Local Similarity | 79.4%;                                                         | Pred. No. 6.8e-13; |                |                   |
|    | Matches 139;          | Conservative                                                   | 0;                 | Mismatches 34; | Indels 2; Gaps 2; |
| QY | 1                     | CTCAAGTCACGCCCT-AAAAGACAGCATGGAATAAATTTGAAATAACAACAAACAGCCTTGC | 59                 |                |                   |
|    |                       |                                                                |                    |                |                   |
|    |                       |                                                                |                    |                |                   |
|    |                       |                                                                |                    |                |                   |
|    |                       |                                                                |                    |                |                   |
| Dd | 26                    | CTCAAGTCACGCCCTCTAAAAGATAGTGGAAATAAATTTGAAATAACAACAAACAGCCTTGC | 85                 |                |                   |
|    |                       |                                                                |                    |                |                   |
|    |                       |                                                                |                    |                |                   |
|    |                       |                                                                |                    |                |                   |
|    |                       |                                                                |                    |                |                   |
| QY | 60                    | TGAAANTTAANATCAGGACTCTCAACCTGCTCCAGTCAGCCTTCCACGAGGCCCTGTCA    | 119                |                |                   |



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||||| 86 TGAATAAACACGAGACACCTGAGCTGCTCCAGTCACGCT-CTCTCAGAAGGCGCTGTCA 144
||||| QY 120 GTACAGTCCCGACCTGTGACTGAGTGTCAGTGCCAGCCAGTGTACCAAGTGTGGT 174
||||| Db 145 GGCAGGGGTAGTACTGCTGAGTGTGAGCAGTGTCGCGCATGTACCAAGTGTAGTG 199

RESULT 7
CNS0091P/c      CNS0091P      925 bp      DNA      linear      GSS 03-JUN-1999
LOCUS           Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION      BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                  fly), genomic survey sequence.
ACCESSION       AL053013      GI:4934461
VERSION         AL053013.1
KEYWORDS        GSS.
SOURCE          Drosophila melanogaster.
ORGANISM        Drosophila melanogaster.
                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                Ephydroidea; Drosophilidae; Drosophila.
REFERENCE       1 (bases 1 to 925)
AUTHORS         Genoscope.
TITLE           Direct Submission
JOURNAL         Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
COMMENT         Determination of this BAC-end sequence was carried out as part of a
                collaboration with the Berkeley Drosophila Genome Project (BDGP).
                The BDGP is constructing a physical map of the Drosophila
                melanogaster genome using these BACs. For further information
                please see http://www.fruitfly.org The BDGP Drosophila
                melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                Aaron Mammosier in Pieter de Jong's laboratory in the Department of
                Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                NY. The library is named RPCI-98 and was constructed by partial
                EcoRI digestion of Drosophila DNA provided by the BDGP from the
                isogenic strain y2; cn bw sp, the same strain used for the BDGP's
                pl and EST libraries. A more detailed description of the library
                and how to order individual BAC clones, the entire library, or
                filters for hybridization from the BACPAC Resource Center can be
                found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES         Location/Qualifiers
                source             1..925
                                /organism="Drosophila melanogaster"
                                /db_xref="taxon:7227"
                                /clone_lib="RPCI-98"
                                /note="end : TET3"
BASE COUNT       120 a      61 c      172 t      511 others
ORIGIN
Query Match      7.4%; Score 47.4; DB 17; Length 925;
Best Local Similarity 11.1%; Pred. No. 0.49;
Matches 37; Conservative 160; Mismatches 136; Indels 0; Gaps 0;

QY 227 CTCGCCAGCAAGGCGGACACCTCTGAGGAGCTCTGAGTGGGAGCAGTGTGCTGT 286
Db 924 SBSCSCSCSBSGSSSSMTSSNSBSCSSSSBSSSTSSMSSSBSSSSSSSSSS 865
QY 287 GCCTCCCTAGAGCTGTAGGCGCCACCGCCACAGAGTCTCTGTAGGCGCAGTGA 346
Db 864 SGTSSACVKNASSCGCCCGNABCCMCSSSSSCGASRGVVKVRASGAGRGGSG 805
QY 347 TGGACCCCTCAACAGCAGGCGCCATCTCCCTCGGAGATATGAGTTGACAGAGACTTGA 406
Db 804 GASASHSSSACBSSSSCSASCSWSSASSSSRSRSGGAGGSGASSSRSSSSSA 745
QY 407 CCGGCTCCCGCAGGACTGTACACGCGCTTGCCTGTGCGCGCAGTGTGCTGACCTACA 466
Db 744 SAGSVYSSASSSSSSSVSCSVSSVSSMSCSBSSSSSASASSSSSSSASCSCCCT 685

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QY 467 GACAGCTCCACATGGACCCCGGGCAACTGGAGCTGCTCTTACCACACAGACTGT 526
Db 684 SWSCSCTSASNSARSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 625
QY 527 CTTCTACCGCGCGCATGCGCATGCGGAGAGGG 559
Db 624 MSSGGGSGSVSSASSGMSVSSSSVSSGSRSSGGG 592

RESULT 8
CNS006DM/c      CNS006DM      997 bp      DNA      linear      GSS 03-JUN-1999
LOCUS           Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION      BACR13C17 of RPCI-98 library from Drosophila melanogaster (fruit
                  fly), genomic survey sequence.
ACCESSION       AL065132      GI:4944302
VERSION         AL065132.1
KEYWORDS        GSS.
SOURCE          Drosophila melanogaster.
ORGANISM        Drosophila melanogaster.
                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                Ephydroidea; Drosophilidae; Drosophila.
REFERENCE       1 (bases 1 to 997)
AUTHORS         Genoscope.
TITLE           Direct Submission
JOURNAL         Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
COMMENT         Determination of this BAC-end sequence was carried out as part of a
                collaboration with the Berkeley Drosophila Genome Project (BDGP).
                The BDGP is constructing a physical map of the Drosophila
                melanogaster genome using these BACs. For further information
                please see http://www.fruitfly.org The BDGP Drosophila
                melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                Aaron Mammosier in Pieter de Jong's laboratory in the Department of
                Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                NY. The library is named RPCI-98 and was constructed by partial
                EcoRI digestion of Drosophila DNA provided by the BDGP from the
                isogenic strain y2; cn bw sp, the same strain used for the BDGP's
                pl and EST libraries. A more detailed description of the library
                and how to order individual BAC clones, the entire library, or
                filters for hybridization from the BACPAC Resource Center can be
                found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES         Location/Qualifiers
                source             1..997
                                /organism="Drosophila melanogaster"
                                /db_xref="taxon:7227"
                                /clone_lib="BACR13C17"
                                /clone_lib="RPCI-98"
                                /note="end : TET3"
BASE COUNT       76 a      145 c      120 g      177 t      479 others
ORIGIN
Query Match      7.3%; Score 47; DB 17; Length 997;
Best Local Similarity 15.5%; Pred. No. 0.62;
Matches 54; Conservative 157; Mismatches 137; Indels 0; Gaps 0;

QY 268 GGTGAGACACTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 327
Db 898 KGKDWGYGTTKMRKBVBABSKBTSCNGBGSGBKSCMBKSSKSYGKGVYCGGSGS 839
QY 328 CTTGTAGGCGCAGTGAAGATGAGACCCCTCAACAGCAGGCGCCATCTCCCTCGGAGATATG 387
Db 838 MVKCKGKCGAGGAGGKGKGGGKGVYKGGCGCGCGGSCVMVMSCKBFGCMKSGCKC 779
QY 388 AGTTGGACAGAGACTTGAACCGGCTCCCGCCAGACCTGTATCCACGCGCCCTGTGCTGTGCC 447
Db 778 VGGGGGGMTAANAANRABAKBKBBSSTBMBMHKCGTCMMWYSTGKSTCSYKBSBG 719
QY 448 CGCACTGCGTCACTACAGCAGCTCCCATGATGACCGCGGGGCAATCTGGAGCTGC 507
Db 718 SBGTTGKSSGSMABBGCBDBKSCCRMAMAYGKKGWKGKBYNKGKSKVVBGTGVBKG 659

```



RESULT 11  
BQ574994/c  
LOCUS  
DEFINITION BQ574994 568 bp mRNA linear EST 19-JUN-2002  
UI-H-E21-bbd-e-09-0-UI.s1 NCI\_CGAP\_Ch2 Homo sapiens cDNA clone  
UI-H-E21-bbd-e-09-0-UI 3', mRNA sequence.  
ACCESSION BQ574994  
VERSION BQ574994  
KEYWORDS BQ574994.1 GI:21478311  
SOURCE EST.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 568)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of  
Orthopedics  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
1..568  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="UI-H-E21-bbd-e-09-0-UI"  
/clone\_lib="NCI\_CGAP\_Ch2"  
/tissue\_type="Chondrosarcoma Grade II"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/note="Organ: Left Pelvis; Vector: p7T3-pac (Pharmacia)  
with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
NCI\_CGAP\_Ch2 is a normalized cDNA library containing the  
following tissue(s): Chondrosarcoma Grade II. The library  
was constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into p7T3-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is  
TGATCAGCT.  
TAG\_LIB=UI-H-E21  
TAG\_TISSUE=grade-2-chondrosarcoma  
TAG\_SEQ=ATCTAATATG  
BASE COUNT 94 a 166 c 174 g 134 t  
ORIGIN

Query Match 6.7%; Score 43; DB 14; Length 568;  
Best Local Similarity 62.6%; Pred. No. 5.2;  
Matches 67; Conservative 0; Mismatches 40; Indels 0; Gaps 0;  
QY 356 CAACAGAGGGCCATCTCCCTGGAGATATGATGGACAGAGACTTGAACCGGCTCC 415  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 383 CAACAAGAGGAGCCTGTCTCCCTGGGGATACAGCATCAACACGACCCCGGATATCC 324  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 416 CCAGGACCTGTACACAGCCGCTGCTGCTGCGCGGACCTGCCTCAGCC 462  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 323 CGTGACCTGCCGGAGGACCGGTGCTGTGTGCTGTGGCTGTGTGAACC 277

RESULT 12  
BQ779177/c

LOCUS BQ779177 440 bp mRNA linear EST 26-JUL-2002  
DEFINITION 946117E05.xl 946 - tassels primordium prepared by Schmidt lab Zea  
mays cDNA, mRNA sequence.  
ACCESSION BQ779177  
VERSION BQ779177.1 GI:21987649  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 440)  
AUTHORS Walbot V.  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
University  
JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: [walbot@stanford.edu](mailto:walbot@stanford.edu)  
Plate: 946117 row: E column: 05.  
Location/Qualifiers  
1..440  
/organism="Zea mays"  
/cultivar="OH43"  
/db\_xref="taxon:4577"  
/clone\_lib="946 - tassels primordium prepared by Schmidt  
lab"  
/tissue\_type="tassels"  
/dev\_stage="just after the transition from vegetative to  
inflorescence development"  
/lab\_host="X10LR"  
/note="Organ: tassels; Vector: HybriZAP; Site\_1: EcoRI;  
Site\_2: XhoI; George Chuck dissected immature tassels  
between 1mm and 3mm. Sharon Stanfield prepared the cDNA  
library in HybriZAP. Sample insert size range was 350 bp  
to 3 Kb with a 1 Kb average."  
BASE COUNT 107 a 132 c 108 g 93 t  
ORIGIN

Query Match 6.6%; Score 42.8; DB 14; Length 440;  
Best Local Similarity 47.7%; Pred. No. 5.6;  
Matches 125; Conservative 0; Mismatches 137; Indels 0; Gaps 0;  
QY 377 CTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCGGACCTGTACACGCCG 436  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 398 CTGGATCGGGCTGGGGACATCGTCTCGTGGGCTCGGACGTACACGAGGACGAGGC 339  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 437 TTGCTGTGCCCCGACTGCGTACAGAGAGGCTCCACATGGACCCCGGGGCAA 496  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 338 CGACGTTATCTCAAGTACATGAACGACGAGCGGCGCTGTCAAGGCTACGGGAGCT 279  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 497 CTGGAGCTGCTTACCAACACAGACTGTCTTACGGGGGCGCATGCCATGGCGGAA 556  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 278 TCTGACAGCTCAGGCTCAACGAGGCGTGCAGCTGATGGGCGCGGAGGAGGAGGA 219  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 557 GGGCACCCCAAGGGCTACTGCTGGAGCGCAGGCTGTACCGTCTTCCCTTAGCTTGT 616  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 218 GGGCAGGACTACATCCAGTTCGAGGACGAGGACATCGACAAGATTTAAGAAATCTGTC 159  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
QY 617 GTGTGTGCGGCCCGCTGTGTATG 638  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 158 CTGCTTACGGCTACCTGTATTG 137  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13  
CNS004NB  
LOCUS  
DEFINITION CNS004NB 839 bp DNA linear GSS 03-JUN-1999  
Drosophila melanogaster genome survey sequence TET3 end of BAC #  
BACR10E16 of RPCI-98 library from Drosophila melanogaster (fruit



REFERENCE 1 (bases 1 to 486)  
 AUTHORS Harvey D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,  
 Lewis, S., and Rubin, G.M.  
 TITLE BDGP/HHMI Drosophila EST Project  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Stapleton, M.  
 BDGP  
 Lawrence Berkeley National Lab  
 One Cyclotron Rd, Berkeley, CA 94720, USA  
 Fax: 510 486 6798  
 Email: <http://www.fruitfly.org/EST>, [est@fruitfly.berkeley.edu](mailto:est@fruitfly.berkeley.edu)  
 Plate: 194 row: F column: 12  
 High quality sequence stop: 343.

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 source  
 1..486  
 /organism="Drosophila melanogaster"  
 /db\_xref="taxon:7227"  
 /clone\_lib="GH19472"  
 /clone\_lib="GH Drosophila melanogaster head pot2"  
 /sex="male and female"  
 /dev\_stage="adult"  
 /lab\_host="DH5 - alpha"  
 /note="Organ: head; Vector: pot2; Site\_1: EcoRI; Site\_2:  
 xhoI; Sized fractionated cDNAs were directly ligated into  
 pot2. plasmid cDNA library."  
 BASE COUNT 64 a 97 c 205 g 119 t 1 others  
 ORIGIN

Query Match 6.6%; Score 42.2; DB 9; Length 486;  
 Best Local Similarity 50.0%; Pred. NO. 8;  
 Matches 104; Conservative 0; Mismatches 104; Indels 0; Gaps 0;  
 QY 394 ACAGAGACTGTGACCGGCTCCCGGAGGCTGTACACGCGCGTGTGCTGTGCGCGGACT 453  
 DB 452 ACCGAGGATTCCCGGACCTCTCCGGAATATCCACCTGATCCAAATCCAGGCGGTACCC 393  
 QY 454 GCCTCAGCCTACAGACAGGCTCCGACATGGACCCCGGGGCAACTCGGAGCTGCTTACC 513  
 DB 392 GATTCCTCCACCGGATGACCACTGTATCCGGAATCCGGGACCGCCACNGAATCGGCTCC 333  
 QY 514 ACAACGAGACTGTCTTCTACCGGCGGCGATGCCATGGCGGAGGCGACCCACAAAGGGCT 573  
 DB 332 ACCTCCAGAAATGACCTCCGCGGAGATCACTCCACCGCCAGCATGGCCACCTGCGAAGGG 273  
 QY 574 ACTGCTGGAGCGCAGGCTGTACCGTGT 601  
 -DB 272 ACCTCTCCGACACACCGCGCTCCAAAGT 245

Search completed: May 12, 2003, 01:55:16  
 Job time : 1074 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 12, 2003, 01:59:44 ; Search time 163 seconds  
(without alignments)  
2224.366 Million cell updates/sec

Title: US-10-037-591A-2

Perfect score: 910

Sequence: 1 MTQVAFVLAAMVMTGYSHW.....ERRLYRVSLACVCRVRVMG 161

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:\*  
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24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID       | Description        |
|------------|-------|-------|--------|----|----------|--------------------|
| 1          | 910   | 100.0 | 504    | 21 | AAA58986 | cDNA encoding a hu |
| 2          | 910   | 100.0 | 504    | 21 | AAA58986 | cDNA encoding a hu |
| 3          | 910   | 100.0 | 504    | 24 | ABA02393 | Human interleukin  |
| 4          | 910   | 100.0 | 644    | 24 | AAD28771 | Human interleukin  |
| 5          | 910   | 100.0 | 644    | 24 | ABA03213 | Human IL-17 recept |
| 6          | 898   | 98.7  | 1320   | 22 | AAS09511 | Human cDNA encodin |
| 7          | 898   | 98.7  | 1320   | 22 | AAC85969 | Native sequence of |
| 8          | 898   | 98.7  | 1320   | 22 | AAF92135 | Human PRO10272 cDN |
| 9          | 834   | 91.6  | 1355   | 23 | AAS35559 | DNA encoding novel |
| 10         | 709   | 77.9  | 985    | 21 | AAA58988 | cDNA encoding a mu |
| 11         | 709   | 77.9  | 985    | 21 | AAA59160 | cDNA encoding a mu |
| 12         | 709   | 77.9  | 985    | 24 | ABA02394 | Murine interleukin |
| 13         | 709   | 77.9  | 1013   | 24 | AAD28772 | Mouse Interleukin- |
| 14         | 693   | 76.2  | 1496   | 24 | AAD28773 | Mouse non-secreted |
| 15         | 493   | 54.2  | 620    | 21 | AAA58987 | cDNA encoding a mu |
| 16         | 493   | 54.2  | 620    | 21 | AAA59159 | cDNA encoding a mu |
| 17         | 167   | 18.4  | 591    | 21 | AAA09153 | Human interleukin- |
| 18         | 167   | 18.4  | 591    | 24 | AAD38083 | Human LP-48 gene.  |
| 19         | 167   | 18.4  | 1047   | 21 | AAA96338 | cDNA encoding a no |
| 20         | 167   | 18.4  | 1047   | 21 | AZ29728  | Human Interleukin  |
| 21         | 167   | 18.4  | 1047   | 22 | AAS46148 | Human DNA encoding |
| 22         | 167   | 18.4  | 1047   | 22 | AAS09510 | Human cDNA encodin |
| 23         | 167   | 18.4  | 1067   | 21 | AZ36836  | Nucleotide sequenc |
| 24         | 167   | 18.4  | 1067   | 23 | AAI67878 | Human interleukin  |
| 25         | 167   | 18.4  | 1107   | 21 | AAA58991 | cDNA encoding a hu |
| 26         | 167   | 18.4  | 1107   | 21 | AAA59149 | cDNA encoding a hu |
| 27         | 167   | 18.4  | 1177   | 22 | AAD15291 | Human interleukin  |
| 28         | 136.5 | 13.9  | 1385   | 21 | AAA58983 | cDNA encoding a hu |
| 29         | 136.5 | 13.9  | 1385   | 21 | AAA59155 | cDNA encoding a hu |
| 30         | 136.5 | 13.9  | 1819   | 21 | AZ52195  | Human transforming |
| 31         | 136.5 | 13.9  | 2361   | 21 | AZ52201  | Human transforming |
| 32         | 125.5 | 13.8  | 540    | 20 | AAH89401 | Human interleukin- |
| 33         | 125.5 | 13.8  | 543    | 21 | AAA58980 | cDNA encoding a hu |
| 34         | 125.5 | 13.8  | 543    | 21 | AAA59152 | cDNA encoding a hu |
| 35         | 125.5 | 13.8  | 687    | 20 | AZ34282  | Human PRO1031 nuc1 |
| 36         | 125.5 | 13.8  | 687    | 21 | AAC78577 | Human PRO1031 (UNQ |
| 37         | 125.5 | 13.8  | 687    | 21 | AAH75694 | cDNA clone DNA5929 |
| 38         | 125.5 | 13.8  | 687    | 21 | AAC58608 | Human PRO1031 prot |
| 39         | 125.5 | 13.8  | 687    | 21 | AZ29727  | Human interleukin  |
| 40         | 125.5 | 13.8  | 687    | 22 | AAS09509 | Human cDNA encodin |
| 41         | 125.5 | 13.8  | 687    | 22 | AAS21466 | Human cDNA sequenc |
| 42         | 125.5 | 13.8  | 687    | 22 | AAC91479 | Human PRO1031 cDNA |
| 43         | 125.5 | 13.8  | 687    | 22 | AAC88961 | Human PRO1031 codi |
| 44         | 125.5 | 13.8  | 689    | 21 | AAA95780 | Human immune syste |
| 45         | 125.5 | 13.8  | 704    | 22 | AAH79255 | Human cell factor- |

ALIGNMENTS

RESULT 1

AAA58986

ID AAA58986 standard; cDNA; 504 BP.

XX AAA58986;

XX 07-NOV-2000 (first entry)

XX cDNA encoding a human interleukin (IL) 174 polypeptide.

XX Interleukin; IL-17; CTIA-8; IL-170; IL-172; IL-173; IL-174; IL-176;

XX IL-177; IL-171; cell proliferation; cancer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT 19..504

XX FT /\*tag= a

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FT      /product= "interleukin-174"
FT      sig_peptide
FT      19..66
FT      /*tag= b
FT      mat_peptide
FT      67..501
FT      /*tag= c
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XX WO200042188-A2.
XX
XX PD 20-JUL-2000.
XX
XX PF 10-JAN-2000; 2000WO-US00006.
XX
XX PR 11-JAN-1999; 99US-0228822.
XX
XX PA (SCHE ) SCHERING CORP.
XX
XX PI Gorman DM, Bazan JF, Kastelein RA;
XX
XX WPI; 2000-466130/40.
XX
XX DR P-PSDB; AAB07598.
XX
XX PT New isolated polynucleotide encoding a mammalian Interleukin-17 like
XX protein used to identify genes for homologous proteins
XX
XX PS Disclosure; Page 16; 11pp; English.
XX
XX CC The present sequence encodes an interleukin-174 (IL-174) polypeptide.
XX The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a
XX member of a new group of interleukins, IL-170 polypeptides. The members
XX comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170
XX protein can be used to treat abnormal proliferation e.g. cancer
XX or degenerative conditions. Antibodies can be used in diagnostic
XX methods to detect over production of IL-170 protein in cells or body
XX fluids.
XX
XX SQ Sequence 504 BP; 98 A; 165 C; 148 G; 93 T; 0 other;

Alignment Scores:
Pred. No.: 3,01e-74 Length: 504
Score: 910.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-10-037-591A-2 (1-161) x ARA58986 (1-504)

QY 1 MetTyrGlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrp 20
DB 19 ATGTACAGGTGTTGTCATTCTTGGCAATGCTATGGGAACCCACACCTACAGCCACTGG 78
QY 21 ProSerCysCysProSerLysGlyGlnAspThrSerGluGluLeuArgTrpSerThr 40
DB 79 CCAGCTGTGCTCCCAAGAGGAGGAGGACCTCTCAGGAGCTGCTGAGGTGGAGCACT 138
QY 41 ValProValProLeuGluProAlaAArgProAsnArgHisProGluSerCysArgAla 60
DB 139 GTCCCTGTGCTCCCTAGAGCTGCTAGGCCCAACCCACCCAGAGTCTCTAGGGCC 198
QY 61 SerGluAspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArg 80
DB 199 AGTGAAGATGGACCCCTCAACAGCAGCGGCCATCTCCCCCTGGAGATATGAGTTGGACAGA 258
QY 81 AspleuAsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysVal 100
DB 259 GACTTGAACCGGTCCCCAGGACCTGTACACGCCCGTGTGCTGTCCCGCACCTGGCTC 318
QY 101 SerLeuGlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsn 120
DB 319 AGCTACAGACAGCTCCCAATGGACCCCGGGGGAACCTCGGAGCTGCTACCAACAC 378
QY 121 GlnThrValPheTyrArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCys 140
DB 121 GlnThrValPheTyrArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCys 140
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Db 379 CAGACTGCTCTTCTACCGGGCCATGCCATGGCGAGAGGGACCCCAAGGGCTACTGC 438
QY 141 LeuGluArgArgLeuTyrArgValSerLeuAlaCysValArgProArgValMet 160
Db 439 CTGGAGCGCAGGCTGTACCGTGTCTTCTAGCTGTGTGTGTCGGGCCCGCTGTGATG 498
QY 161 Gly 161
Db 499 GGC 501

RESULT 2
AAA59158
ID AAA59158 standard; cDNA; 504 BP.
XX
XX AC AAA59158;
XX
XX DT 07-NOV-2000 (first entry)
XX
XX DE cDNA encoding a human interleukin-174 polypeptide.
XX
XX KW Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;
XX IL-174; IL-176; IL-177; cell proliferation; cancer; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX CDS 19..504
XX FT /*tag= a
XX FT /product= "interleukin-174"
XX FT sig_peptide 19..66.
XX FT /*tag= b
XX FT mat_peptide 67..501
XX FT /*tag= c
XX
XX PN WO200042187-A1.
XX
XX PD 20-JUL-2000.
XX
XX PF 10-JAN-2000; 2000WO-US00005.
XX
XX PR 11-JAN-1999; 99US-0229402.
XX
XX PA (SCHE ) SCHERING CORP.
XX
XX PI Gorman DM, Bazan JF, Kastelein RA;
XX
XX WPI; 2000-476060/41.
XX P-PSDB; AAB07692.
XX
XX PT New DNA sequence encoding a mammalian homolog of CTLA-8, designated
XX interleukin-171 (IL-171), useful for recombinant production of IL-171
XX which can be used for treating conditions associated with abnormal
XX physiology or development.
XX
XX PS Disclosure; Page 19; 11pp; English.
XX
XX CC The present sequence encodes an interleukin (IL)-174 polypeptide.
XX It is a mammalian homologue of the cytokine designated CTLA-8 (also
XX referred to as IL-17). The specification also describes homologues
XX IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA
XX sequence encoding IL-171 is useful for identifying genes, mRNA and
XX cDNA molecules which code for related or homologous proteins. The
XX IL-171 protein, antibodies against IL-171, and compounds which have
XX binding affinity to IL-171 are useful in treatment of conditions
XX associated with abnormal physiology or development, including abnormal
XX proliferation, e.g. cancerous conditions, or degenerative conditions.
XX The IL-171 protein can be used in kits and assay methods for identifying
XX compounds that selectively bind to IL-171.
XX
XX SQ Sequence 504 BP; 98 A; 165 C; 148 G; 93 T; 0 other;

Alignment Scores:
Pred. No.: 3,01e-74 Length: 504
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Score: 910.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0

US-10-037-591A-2 (1-161) x ABA02393 (1-504)

QY 1 MetTyrGlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrp 20  
Db 19 ATGTACCAGGTGGTTCATTCTGGCAATGTCATGGAAACCCACCTACAGCCACTGG 78  
QY 21 ProSerCysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThr 40  
Db 79 CCCAGCTGCTGCCCCAGCAAGGGCAGACACCTCTGAGGAGCTGCTGAGGTGGAGCACT 138  
QY 41 ValProValProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAla 60  
Db 139 GTGCCTGTGCTCCCTAGAGCCTGCTAGGCCCAACCCGCCACAGAGTCTGTAGGGCC 198  
QY 61 SerGluAspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArg 80  
Db 199 AGTGAAGATGACCCCTCCACAGCAGGCGCATCTCCCTCGAGATATGAGTTGGACAGA 258  
QY 81 AspLeuAsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysVal 100  
Db 259 GACTTGAACCGGCTCCCCAGGACCTGTACACACGCCGCTTGCCTGGCCGCACTGGCTC 318  
QY 101 SerLeuGlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsn 120  
Db 319 AGCCTACAGACAGCTCCACATGACGCCCGGGGCACTCGGAGCTGCTCTACCCACAAC 378  
QY 121 GlnThrValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCys 140  
Db 379 CAGACTGCTCTTACCGCGGCCATGCTCCATGGCAGAGGCGACCCACAGGGCTACTGC 438  
QY 141 LeuGluArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMet 160  
Db 439 CTGGAGCGCAGGCTGTACCGGTTCCTTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTG 498  
QY 161 Gly 161  
Db 499 GGC 501

## RESULT 3

ABA02393  
ID ABA02393 standard; DNA; 504 BP.

XX AC ABA02393;

XX DT 26-FEB-2002 (first entry)

XX DE Human interleukin 174 (IL-174)-encoding DNA.

XX KW Human; interleukin 174; IL-174; cytokine; Th2 response;  
KW innate immune response; inflammation; gut cell growth;  
KW extramedullary haematopoiesis; antibody response; granuloma formation;  
KW autoimmune condition; multiple sclerosis; systemic lupus erythematosus;  
KW rheumatoid arthritis; diabetes; psoriasis; infectious agent;  
KW inflammatory condition; Crohn's disease; ulcerative colitis;  
KW pancreaticitis; hepatitis; allergy; Th2-mediated condition;  
KW systemic anaphylactic response; skin hypersensitivity response;  
KW dermatitis; asthma; fibrosis; eosinophilic gastritis; immunomodulator;  
KW antiinflammatory; antiarthritic; antidiabetic; antifungal;  
KW dermatological; neuroprotective; anti-allergic; agonist; antagonist; ds.

OS Homo sapiens.

XX FH Key Location/Qualifiers  
XX CDS 19..504

FT FT /\*tag= a  
FT FT /product= "Human IL-174"  
FT sig\_peptide 19..66

FT mat\_peptide /\*tag= b  
FT 67..501 /\*tag= c  
FT /\*product= "Mature human IL-174"  
XX

PN WO200179288-A2.

XX 25-OCT-2001.

XX 17-APR-2001; 2001WO-US12493.

XX 18-APR-2000; 2000US-198488P.

XX (SCHE ) SCHERING CORP.

PI Hurst SD, Zurawski SM, Rennick DM;

XX WPI; 2002-034343/04.

XX P-PSDB; AAM52691.

XX Administering an interleukin 174 agonist or antagonist to a mammal  
regulates various immune and inflammatory responses and is useful to  
treat for example autoimmune diseases, allergies or response to an  
infection

XX Disclosure; Page 26-27; 29pp; English.

XX The invention relates to methods of directing an immune response in a  
mammal by the administration of an agonist or antagonist of the cytokine  
interleukin 174 (IL-174). Administration of an IL-174 agonist directs the  
immune response towards a Th2 response, stimulates an innate immune  
response, augments the inflammatory response from epithelial or  
fibroblast cells, induces gut cell growth, promotes extramedullary  
haematopoiesis, or augments an antibody response in serum and faecal  
material, while administration of an IL-174 antagonist directs the immune  
response away from a Th2 type response, and prevents inflammation or  
granuloma formation. IL-174 agonists may be used to treat autoimmune  
conditions (particularly multiple sclerosis, systemic lupus  
erythematosus, rheumatoid arthritis, diabetes or psoriasis), a response  
to an infectious agent, or inflammatory conditions such as Crohn's  
disease, ulcerative colitis, pancreatitis, or hepatitis. IL-174  
antagonists may be used to treat inflammatory, allergic or Th2-mediated  
conditions (e.g., systemic anaphylactic response, skin hypersensitivity  
response, dermatitis, asthma, fibrosis, or eosinophilic gastritis). The  
present sequence represents DNA encoding human IL-174.

XX SQ Sequence 504 BP; 98 A; 165 C; 148 G; 93 T; 0 other;

## Alignment Scores:

Pred. No.: 3 01e-74 Length: 504  
Score: 910.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0

US-10-037-591A-2 (1-161) x ABA02393 (1-504)

QY 1 MetTyrGlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrp 20

Db 19 ATGTACCAGGTGGTTCATTCTGGCAATGTCATGGAAACCCACCTACAGCCACTGG 78

QY 21 ProSerCysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThr 40

Db 79 CCCAGCTGCTGCCCCAGCAAGGGCAGACACCTCTGAGGAGCTGCTGAGGTGGAGCACT 138

QY 41 ValProValProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAla 60

Db 139 GTGCCTGTGCTCCCTAGAGCCTGCTAGGCCCAACCCGCCACAGAGTCTGTAGGGCC 198

QY 61 SerGluAspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArg 80

Db 199 AGTGAAGATGGACCCCTCAACAGCAGGGCCATCTCCCTGGAGATATGATGGACAGA 258



QY 81 AspLeuAsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysVal 100  
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Db 259 GACTGAACGGCTCCCGCAGGACCTGTACACCGCGTTCCTGTGCGCGCTGGGTC 318  
  
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Db 319 AGCCTACAGACAGGCTCCACATGGACCGCGGCAACTCGGAGCTGCTTACCAAC 378  
  
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Db 379 CAGACTGTCTTACCGCGCGCGCATGCGTGGAGAGGCGACCCACAGGGCTACTGC 438  
  
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Db 439 CTGAGCGCAGGCTGTACCGTGTTCCTTAGCTGTGTGTGTGCGCGCGCTGTGATG 498  
  
QY 161 Gly 161  
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Db 499 GGC 501

## RESULT 4

AAD28771  
ID AAD28771 standard; cDNA; 644 BP.

XX AAD28771;

DT 07-MAY-2002 (first entry)

DE Human Interleukin-17 like (IL-17L) cDNA.

XX Human; interleukin-17 like; IL-17L; immune system dysfunction; diabetes;  
KW cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;  
KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;  
KW autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;  
KW infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;  
KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;  
KW eczema; psoriasis; wound healing; osteoporosis; Paget's disease;  
KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;  
KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;  
KW cancer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 159..644

FT /\*tag- a

FT /product- "Human IL-17L protein"

FT 159..206

FT /\*tag- b

FT 207..641

FT /\*tag- c

FT /product- "Mature IL-17L protein"

XX W0200208285-A2.

PN 31-JAN-2002.

XX 21-JUN-2001; 2001WO-US19861.

XX 22-JUN-2000; 2000US-213125P.

PR 02-FEB-2001; 2001US-266159P.

PR 16-MAR-2001; 2001US-0810384.

XX (AMGE-) AMGEN INC.

XX Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S;

PI WPI; 2002-155217/20.

XX P-PSDB; AAE18120.

XX Nucleic acid molecules encoding Interleukin 17 (IL-17) - like

XX polypeptides useful in the treatment, prevention and diagnosis of

PT

PT diseases e.g. cancer

XX Claim 1; Fig 1; 242pp; English.

XX The invention relates to nucleic acid molecules encoding Interleukin 17

CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels  
CC of IL-17 protein in an animal. The IL-17 protein is useful for treating,  
CC preventing or ameliorating a disease, such as immune system dysfunction  
CC (rheumatoid arthritis, osteoarthritis, inflammatory joint disease);  
CC autoimmune multiple sclerosis, lupus, diabetes, inflammatory bowel  
CC disease, transplant rejection, graft vs. host disease; infections (HIV,  
CC hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,  
CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung  
CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin  
CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone  
CC (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy  
CC atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma  
CC leukaemia); reproductive (infertility, miscarriage, endometriosis), eye  
CC (blindness, retinal neuropathy) and treatment of diseases involving  
CC inflammation. The present sequence is human Interleukin-17 like (IL-17L)  
CC cDNA.

SQ Sequence 644 BP; 144 A; 204 C; 173 G; 123 T; 0 other;

## Alignment Scores:

Pred. No.: 4,1e-74 Length: 644  
Score: 910.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0

US-10-037-591A-2 (1-161) x AAD28771 (1-644)

QY 1 MetTyrGlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrp 20

Db 159 ATGTACAGGCTGGTGTGATCTTGGCAATGTCATGGGAACCCACCTACAGCCACTGG 218

QY 21 ProSerCysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThr 40

Db 219 CCCAGCTGCTGCCCCAGCAAGGGCAGGACACCTCTGAGGAGCTCTGAGGTGGAGCACT 278

QY 41 ValProValProProLeuGluProAlaArgProAlaArgHisProGluSerCysArgAla 60

Db 279 GTGCTGTGCTCCCTAGAGCCTGTAGGCCCAACCCAGAGTCTGTAGGGGCC 338

QY 61 SerGluAspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArg 80

Db 339 AGTGAAGATGGACCCCTCAACAGCAGGAGGCCATCTCCCTGGAGATATGAGTTGGACAGA 398

QY 81 AspLeuAsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysVal 100

Db 399 GACTTGAACCGCTCCCGCAGGACCTGTACAGGCCGCTGCTGCTGCCCGCACTGCGTC 458

QY 101 SerLeuGlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsn 120

Db 459 AGCCTACAGACAGGCTCCACATGGACCCCGGGGCACACTCGGAGCTGCTTACCAACAC 518

QY 121 GlnThrValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCys 140

Db 519 CAGACTGTCTTCTACCGCGCGCCATGCGCATGGCAGAGAGGGGCCACACCAAGGGCTACTGC 578

QY 141 LeuGluArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMet 160

Db 579 CTGGAGCGCAGGCTGCTACCGTGTTCCTTAGCTGTGTGTGTGCGGCCCGCTGTGATG 638

QY 161 Gly 161

Db 639 GGC 641

## RESULT 5

ABAO3213

ID ABA03213 standard; cDNA; 644 BP.

XX AC ABA03213;  
XX DT 11-FEB-2002 (first entry)  
XX DE Human IL-17 receptor like protein ligand, IL-17E, coding sequence.  
XX KW Human; IL-17 receptor-like protein; immunomodulatory; antiarthritic;  
KW antipsoriatic; antimicrobial; anorectic; nootropic; neuroprotective;  
KW antiasthmatic; antiallergic; dermatological; cytostatic; gene therapy;  
KW interleukin 17; immune system disorder; infection; weight; reproductive;  
KW neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation;  
KW glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;  
KW tumour; IL-17E; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 159..644  
FT FT /\*tag= a  
FT FT /product= "Human IL-17E"  
XX PN WO200168705-A2.  
XX XX 20-SEP-2001.  
XX XX 16-MAR-2001; 2001WO-US08688.  
XX XX 16-MAR-2000; 2000US-189923P.  
XX XX 12-MAY-2000; 2000US-204208P.  
XX XX 27-NOV-2000; 2000US-072323.  
XX XX 02-FEB-2001; 2001US-266159P.  
XX XX (AMGE-) AMGEN INC.  
XX PI Jing S, Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ;  
XX WPI: 2002-055100/07.  
XX DR P-PSDB: AAM47464.  
XX XX  
XX PT Three human nucleic acids encoding interleukin 17 (IL-17) receptor like  
PT polypeptides, useful for treating, diagnosing, ameliorating or  
PT preventing immune system disorders (e.g. psoriatic arthritis) and  
PT infections (e.g. viral infections).  
XX XX  
XX PS Example 9; Page 233-234; 239pp; English.  
XX CC The present invention relates to novel human nucleic acids encoding  
CC interleukin 17 (IL-17) receptor like proteins (see ABA03200-ABA03202,  
CC AAM47456, AAM47458 and AAM47459). The IL-17 receptor-like proteins and  
CC coding sequences are useful for treating a pathological condition related  
CC to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g.  
CC viral infections), weight disorders (e.g. obesity), neuronal dysfunction  
CC disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin  
CC disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis),  
CC bone disease (e.g. osteoporosis), vascular system disorders (e.g.  
CC ischaemia), eye disorders, reproductive disorders, tumours and  
CC inflammation. The present sequence is the coding sequence for IL-17E, a  
CC human IL-17 receptor like protein ligand.  
XX XX  
XX SQ Sequence 644 BP; 144 A; 204 C; 173 G; 123 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 4,1e-74 Length: 644  
Score: 910.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
  
US-10-037-591A-2 (1-161) x ABA03213 (1-644)  
QY 1 MetTyrGlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrp 20

Db 159 ATGTACAGGTGGTTCATTTGGCAATGTCATGGAAACCCACACCTACAGCCACTGG 218  
QY 21 ProSerCysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTyrSerThr 40  
Db 219 CCCAGTGTCTGCCCCAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 278  
QY 41 ValProValProLeuGluProAlaAaGProAsnArghisProGluSerCysArgAla 60  
Db 279 GTGCGCTGTGCTCCCTAGAGCTGTAGGCCCAACCGCCACAGAGTCTCTGTAGGGCC 338  
QY 61 SerGluAspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArg 80  
Db 339 ACTGAAGATGGACCCCTCAACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 398  
QY 81 AspLeuAsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysVal 100  
Db 399 GACTTGACCGGCTCCCGCAGGACCTGTACACGCGCGTGTGCTGCGCCGACTGCGTC 458  
QY 101 SerLeuGlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsn 120  
Db 459 AGCCTACAGACAGGCTCCACATGGACCCCGGGGCACTCGGAGGCTGCTCTACCAAC 518  
QY 121 GlnThrValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCys 140  
Db 519 CAGACTGTCTTCTACCGCGGCGCATGCCATGGCGAGAGGGCACCACCAAGGCGTACTGC 578  
QY 141 LeuGluArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMet 160  
Db 579 CTGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 638  
QY 161 Gly 161  
Db 639 GGC 641  
  
RESULT 6  
AAS09511  
ID AAS09511 standard; cDNA; 1320 BP.  
XX AC AAS09511;  
XX DT 24-OCT-2001 (first entry)  
XX DE Human cDNA encoding Interleukin 17E ligand, IL-17E.  
XX KW Human; Interleukin-17E ligand; IL-17E; agonist; antagonist; ss;  
KW PRO10272; DNA 147531-2821; systemic lupus erythematosus;  
KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;  
KW allergic disease; asthma; demyelinating disease;  
KW degenerative cartilaginous disorder; transplantation associated disease.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 259..791  
FT FT /\*tag= a  
FT FT /product= "IL-17E"  
FT FT sig\_peptide 259..357  
FT FT /\*tag= b  
FT FT mat\_peptide 358..788  
FT FT /\*tag= c  
FT FT /label= Mature\_IL-17E  
XX PN WO200146420-A2.  
XX PD 28-JUN-2001.  
XX XX 20-DEC-2000; 2000WO-US34956.  
XX PR 23-DEC-1999; 99US-0172096.  
XX PR 30-DEC-1999; 99WO-US31274.  
XX PR 11-JAN-2000; 2000US-0175481.  
XX PR 18-FEB-2000; 2000WO-US04341.

PR 02-MAR-2000; 2000WO-US05841.  
 PR 21-MAR-2000; 2000US-0191007.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 22-JUN-2000; 2000US-0213087.  
 PR 22-AUG-2000; 2000US-0644848.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 24-OCT-2000; 2000US-0242837.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 28-NOV-2000; 2000US-0253646.  
 PR 01-DEC-2000; 2000WO-US32678.

(GETH ) GENENTECH INC.

PI Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;  
 PI Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RL;  
 PI Watanabe CK, Williams PM, Wood WI, Yansura DG;

DR WPI; 2001-451708/48.  
 DR P-PSDB; AAU04932.

XX Novel PRO polypeptides homologous to interleukin-17, useful for the  
 PT diagnosis and treatment of immune related disease e.g. rheumatoid  
 PT arthritis and diabetes

XX Claim 1; Fig 5; 188pp; English.

XX The sequence (DNA 147531-2821) encodes a PRO polypeptide (PRO10272)  
 CC which is the human Interleukin 17E ligand, IL-17E. A composition  
 CC containing ant/agonists to the PRO polypeptides or individual components  
 CC are useful for treating a mammal with an immune related disease, e.g.  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 CC disease, contact dermatitis, an allergic disease e.g. food  
 CC hypersensitivity, asthma, a transplantation associated disease, or a  
 CC chronic inflammatory demyelinating polyneuropathy. Treating a  
 CC degenerative cartilaginous disorder comprises administering a PRO1031 or  
 CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous  
 CC examples of the diseases and disorders are given in the specification.

XX Sequence 1320 BP; 280 A; 353 C; 384 G; 303 T; 0 other;

#### Alignment Scores:

Pred. No.: 1.27e-72 Length: 1320  
 Score: 898.00 Matches: 159  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.68% Indels: 0  
 DB: 22 Gaps: 0

US-10-037-591A-2 (1-161) x AAS09511 (1-1320)

QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22  
 DB 313 CAGGTGGTTGATCTTGGCAATGGTCATGGACCCACACCTACAGCCACTGGCCGAC 372  
 QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42  
 DB 373 TGTGCCCCCAGCAAGGGCAGGACACCTCTCAGGAGCTGCTGAGGTGGAGCACTGTGCT 432  
 QY 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62  
 DB 433 CTGGCTCCCTAGAGCTGTGTCAGGCCAACCCGCCACAGAGTCTCTAGGGCCAGTGAA 492  
 QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu 82  
 DB 493 GATGACCCCTCAACAGCAGGCGCCATCTCCCTGGAGATATGATTGGACAGACACTTG 552  
 QY 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102

Db 553 AACGGGTCCCCCAGGACCTGTACACGCCCTTGCTGTGCTGCCGCACTGGCTAGCCTA 612  
 QY 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122  
 Db 613 CAGACAGCTCCCACTGACGACCCCGGGCAACTCGGAGCTGCTTACCACACACAGACT 672  
 QY 123 ValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142  
 Db 673 GTCTTCTACAGCGCGCCATGCCATGGCGAGAGGCGACCCACAGGGCTACTGCTGGAG 732  
 QY 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161  
 Db 733 CGCAGGCTGTACCGTGTTCCTTAGCTGTGTGTGCGGCCGCCGCTGTGATGATG 789

#### RESULT 7

AAC85969

ID AAC85969 standard; cDNA; 1320 BP.

XX AAC85969;

XX 22-AUG-2001 (first entry)

XX Native sequence of PRO10272 cDNA, clone DNA147531-2821..

XX PRO; PRO1081; PRO1274; PRO10272; proliferation; T-lymphocyte;  
 KW PRO199; PRO1556; PRO4401; PRO10268; inhibition; stimulation;  
 KW infiltration; mononuclear cell; eosinophil; erythema multiforme;  
 KW polymorphonuclear neutrophil; PMN; antibody; immune-related disorder;  
 KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;  
 KW juvenile chronic arthritis; spondyloarthropathy; systemic sclerosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; skin disease;  
 KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia; asthma;  
 KW autoimmune thrombocytopaenia; thyroiditis; diabetes mellitus; allergy;  
 KW immune-mediated renal disease; demyelination; central nervous system;  
 KW peripheral nervous system; idiopathic demyelinating polyneuropathy;  
 KW Guillain-Barre syndrome; hepatobiliary disease; eosinophilic pneumonia;  
 KW chronic active hepatitis; sclerosing cholangitis; allergic rhinitis;  
 KW granulomatous bowel disease; gluten-sensitive enteropathy; urticaria;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy; contact dermatitis;  
 KW Whipple's disease; idiopathic pulmonary fibrosis; contact dermatitis;  
 KW psoriasis; atopic dermatitis; hypersensitivity pneumonitis;  
 KW graft rejection; graft-versus-host disease; ss.

Homo sapiens.

| Key         | Location/Qualifiers              |
|-------------|----------------------------------|
| CDS         | 259..792                         |
|             | /*tag= a                         |
| sig_peptide | /product= "PRO10272 polypeptide" |
|             | 259..354                         |
|             | /*tag= b                         |
| mat_peptide | 355..769                         |
|             | /*tag= c                         |

WO200140465-A2.

07-JUN-2001.

10-NOV-2000; 2000WO-US30873.

30-NOV-1999; 99WO-US28313.

09-DEC-1999; 99US-0170262.

23-DEC-1999; 99US-0172059.

11-JAN-2000; 2000US-0175481.

20-JAN-2000; 2000US-0177118.

18-FEB-2000; 2000WO-US04342.

03-MAR-2000; 2000US-0187202.

30-MAY-2000; 2000WO-US14941.

05-JUN-2000; 2000US-0209832.

24-AUG-2000; 2000WO-US23328.

(GETH ) GENENTECH INC.

XX Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ:  
 PI Tamas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI: 2001-381384/40.  
 DR P-PSDB; AAB47299.  
 XX  
 PT Isolated PRO polypeptide useful for treat or diagnose an immune-related  
 PT disorder e.g. arthritis, asthma, allergy, diabetes or psoriasis -  
 XX  
 PS Claim 2; Fig 17; 124pp; English.  
 XX  
 CC The sequences given in AAC85961-69 encode PRO polypeptides. PRO1081,  
 CC PRO1274 and PRO10272 stimulate the proliferation of T-lymphocytes and  
 CC PRO1199, PRO1556, and PRO10268 inhibit the proliferation of  
 CC T-lymphocytes. PRO1754 and PRO9912 act to enhance the infiltration of  
 CC mononuclear cells, eosinophils or polymorphonuclear neutrophils (PMN)  
 CC into the tissue of a mammal. The PRO cDNA's and antibodies which  
 CC bind to them, are used to treat an immune-related disorder in a  
 CC mammal. Such disorders include systemic lupus erythematosus,  
 CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a  
 CC spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory  
 CC myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,  
 CC autoimmune hemolytic anaemia, autoimmune thrombocytopenia, thyroiditis,  
 CC diabetes mellitus, immune-mediated renal disease, a demyelinating  
 CC disease of the central or peripheral nervous system, idiopathic  
 CC demyelinating polynuropathy, Guillain-Barre syndrome, a chronic  
 CC inflammatory demyelinating polynuropathy, a hepatobiliary disease,  
 CC infectious or autoimmune chronic active hepatitis, primary biliary  
 CC cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an  
 CC allergic disease, asthma, allergic rhinitis, atopic dermatitis, food  
 CC hypersensitivity, urticaria, an immunologic disease of the lung,  
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
 CC pneumonitis, a transplantation associated disease, graft rejection or  
 CC graft-versus-host disease.  
 XX  
 SQ Sequence 1320 BP; 280 A; 353 C; 384 G; 303 T; 0 other;

Alignment Scores:  
 Pred. No.: Length: 1320  
 Score: 898.00 Matches: 159  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.68% Indels: 0  
 DB: 22 Gaps: 0

US-10-037-591A-2 (1-161) x AAC85969 (1-1320)

QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22  
 DB 313 CAGGTGGTGGTTCATCTTGGCAATGGTCAATGGAACCCACACTACAGGCACCTGGCCAGC 372  
 QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42  
 DB 373 TGCTGCCCCACCAAGGCGCAGACACCTCTCAGGAGCTGCTGAGTGGAGCACTGTGCTT 432  
 QY 43 ValProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62  
 DB 433 GTGCTCCCTCCTAGAGCTCTAGGCCCAACGCCACCCAGAGCTCTGTAGGCCCACTGAA 492  
 QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu 82  
 DB 493 GATGACCCCTCAACAGCAGGCGCATCTCCCTGGAGATATGATGGACAGAGACTTG 552  
 QY 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102  
 DB 553 AACCGGCTCCCCAGGACCTGTACACGCCCTGTGCTGCTGCCGCCACTGGCTGAGCCTA 612  
 QY 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122

DB 613 CAGACAGGCTCCACATGACGCCCGGGCACTCGAGCTGTCTTACCACAACAGACT 672  
 QY 123 ValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142  
 DB 673 GTCCTTACAGGCGCATGCTGCGGAGAGGACCCACCAAGGCTACTGCTGCTGAG 732  
 QY 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161  
 DB 733 CGCAGGCTGACCGTCTTCTTCCCTAGCTGTGTGTGTGCGGCCCGCTGTGATGGC 789

RESULT 8  
 AAF92135  
 ID AAF92135 standard; cDNA; 1320 BP.  
 XX  
 AC AAF92135;  
 XX  
 DT 15-MAY-2001 (first entry)  
 XX  
 DE Human PRO10272 cDNA.  
 XX  
 KW Human; PRO protein; mapping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200116318-A2.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 24-AUG-2000; 2000WO-US23328.  
 XX  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 07-DEC-1999; 99US-0169495.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 11-JAN-2000; 2000US-0175481.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 01-MAR-2000; 2000US-05601.  
 PR 03-MAR-2000; 2000US-0187202.  
 PR 25-APR-2000; 2000US-0193397.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 05-JUN-2000; 2000US-0209832.  
 XX  
 (GETH ) GENENTECH INC.  
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;  
 XX  
 DR WPI: 2001-183260/18.  
 DR P-PSDB; AAB87603.  
 XX  
 PT Eighty four nucleic acids encoding PRO polypeptides, useful in  
 PT molecular biology, including use as hybridization probes, and in  
 PT chromosome and gene mapping.  
 XX  
 PS Claim 2; Fig 155; 278pp; English.  
 XX  
 CC The present sequence is the coding sequence for a human PRO polypeptide  
 CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO  
 CC antagonists or anti-PRO antibodies are useful for preparation of a  
 CC medicament useful in the treatment of a condition which is responsive to  
 CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO  
 CC protein may also be employed as molecular weight markers for protein  
 CC electrophoresis. The PRO coding sequence has applications in molecular  
 CC biology, including use as hybridisation probes, and in chromosome and  
 CC gene mapping.  
 XX  
 SQ Sequence 1320 BP; 280 A; 353 C; 384 G; 303 T; 0 other;

Alignment Scores:  
 Pred. No.: Length: 1320  
 Score: 898.00 Matches: 159



```

RESULT 10
AAA58988
ID AAA58988 standard; cDNA; 985 BP.
XX
AC AAA58988;
XX
DT 07-NOV-2000 (first entry)
XX
DE cDNA encoding a murine interleukin (IL) 174 polypeptide.
XX
KW Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;
KW IL-177; IL-171; cell proliferation; cancer; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..510
FT sig_peptide /tag= a
FT mat_peptide /tag= b
FT /tag= c
XX
PN WO200042188-A2.
XX
PD 20-JUL-2000.
XX
PF 10-JAN-2000; 2000WO-US00006.
XX
PR 11-JAN-1999; 99US-0228822.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Gorman DM, Bazan JF, Kastelein RA;
XX
DR WPI; 2000-466130/40.
XX
DR P-PSDB; AAB07600.
XX
PT New isolated polynucleotide encoding a mammalian Interleukin-17 like
PT protein used to identify genes for homologous proteins -
XX
PS Disclosure; Page 18; l1lpp; English.
XX
CC The present sequence encodes an interleukin-174 (IL-174) polypeptide.
CC The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a
CC member of a new group of interleukins, IL-170 polypeptides. The members
CC comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170
CC protein can be used to treat abnormal proliferation e.g. cancer
CC or degenerative conditions. Antibodies can be used in diagnostic
CC methods to detect over production of IL-170 protein in cells or body
CC fluids.
XX
SQ Sequence 985 BP; 199 A; 296 C; 268 G; 222 T; 0 other;

Alignment Scores:
Pred. No.: 1,55e-55 Length: 985
Score: 709.00 Matches: 129
Percent Similarity: 82.14% Conservative: 9
Best Local Similarity: 76.79% Mismatches: 22
Query Match: 77.91% Indels: 8
DB: 21 Gaps: 1

US-10-037-591A-2 (1-161) x AAA58988 (1-985)
Oy 1 MetTyrGlnValAlaPheLeuAlaMetValMetGlyThrHisThrTyr----- 17
Db 1 ATGTACCAAGGCTGTTCATCTTGGCATATGTCGGGAAACCCACACCTCAGCTGCGG 60
Oy 18 -----SerHisTyrProSerCysCysProSerLysGlyGlnAspThrSer 32
Db 61 ATCCAGGAGGCTGCAGTCACCTTGGCCAGCTGCTCCCGCAGGCAAGAGCAGAACCCCGG 120

33 GluGluLeuLeuArgTyrSerThrValProValProLeuGluProAlaArgProAsn 52
121 GAGAGTGGCTGAAGTGGAGCTTCGATCTGTGTCCCGCCAGAGCCCTCTGAGCCACACC 180
53 ArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIleSer 72
181 CACCAGCAGAAATCCTGCAGGGCCAGCAAGGATGCGCCCTCAACAGCAGGCGCATCTCT 240
73 ProTyrArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrHisAla 92
241 CCTTGGAGCTATGAGTTGGACAGGACTTGAATCGGTGCCCGGAGGACCTGTACCACGCT 300
93 ArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArgGly 112
301 CGATGCTGTGCGCCACACTGCGTCAGCTACAGACAGGCTCCACATGGACCCGCTGGGC 360
113 AsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArgProCysHisGlyGlu 132
361 AACTCGCTCCACTTTTACCACACACACGCGTCTTCTACCGGGCGCATGCCATGGTCAG 420
133 LysGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyrArgValSerLeuAlaCys 152
421 GAAGGTACCATCGCGCTACTGCTTGGAGCGCAGGCTCTACCGAGTCTCCTTGGCTTGT 480
153 ValCysValArgProArgValMet 160
481 GTGTGTGCGCGCCCGGGTCATG 504

RESULT 11
AAA59160
ID AAA59160 standard; cDNA; 985 BP.
XX
AC AAA59160;
XX
DT 07-NOV-2000 (first entry)
XX
DE cDNA encoding a murine interleukin-174 polypeptide.
XX
KW Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;
KW IL-174; IL-176; IL-177; cell proliferation; cancer; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..510
FT /tag= a
FT /product= "interleukin-174"
FT sig_peptide 1..48
FT /tag= b
FT mat_peptide 49..507
FT /tag= c
XX
PN WO200042187-A1.
XX
PD 20-JUL-2000.
XX
PF 10-JAN-2000; 2000WO-US00005.
XX
PR 11-JAN-1999; 99US-0229402.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Gorman DM, Bazan JF, Kastelein RA;
XX
DR WPI; 2000-476060/41.
XX
DR P-PSDB; AAB07694.
XX
PT New DNA sequence encoding a mammalian homolog of CTLA-8, designated
PT interleukin-171 (IL-171), useful for recombinant production of IL-171
PT which can be used for treating conditions associated with abnormal
PT physiology or development -
XX
PS Disclosure; Page 21; l1lpp; English.
```

XX The present sequence encodes an interleukin (IL)-174 polypeptide.  
 CC It is a mammalian homologue of the cytokine designated CTLA-8 (also  
 CC referred to as IL-17). The specification also describes homologues  
 CC IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA  
 CC sequence encoding IL-171 is useful for identifying genes, mRNA and  
 CC cDNA molecules which code for related or homologous proteins. The  
 CC IL-171 protein, antibodies against IL-171, and compounds which have  
 CC binding affinity to IL-171 are useful in treatment of conditions  
 CC associated with abnormal physiology or development, including abnormal  
 CC proliferation, e.g. cancerous conditions, or degenerative conditions.  
 CC The IL-171 protein can be used in kits and assay methods for identifying  
 CC compounds that selectively bind to IL-171.

XX SQ Sequence 985 BP; 199 A; 296 C; 268 G; 222 T; 0 other;

Alignment Scores:  
 Pred. No.: 1.55e-55 Length: 985  
 Score: 709.00 Matches: 129  
 Percent Similarity: 82.14% Conservative: 9  
 Best Local Similarity: 76.79% Mismatches: 22  
 Query Match: 77.91% Indels: 8  
 DB: 21 Gaps: 1

US-10-037-591A-2 (1-161) x AAA59160 (1-985)

Qy 1 MetTyrGlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyr----- 17  
 Db 1 ATGTACCAAGCTGTGTCATCTTGGCATGATCGTGGGAGCCACACCGTCAGCTGCGG 60  
 Qy 18 -----SerHisTrpProSerCysCysProSerLysGlyGlnAspThrSer 32  
 Db 61 ATCCAGGAGGGTGCAGTCACCTGTCGCCAGCTGCTGCCAGCAAGAGCAAGACCCCG 120  
 Qy 33 GluGluLeuLeuArgTrpSerThrValProValProLeuProLeuGluProAlaArgProAsn 52  
 Db 121 GAGGAGTGGCTGAATGGAGCTGCATCTGTGTCTCCCGCCAGAGCCCTCTGACCCACACC 180  
 Qy 53 ArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIleSer 72  
 Db 181 CACACGCGAGAATCTCTGAGGCCAGCAAGATGCGCCCTCAACAGCAGGCGCATCTCT 240  
 Qy 73 ProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrHisAla 92  
 Db 241 CTTGGAGCTATGAGTTGACAGGAGCTTGAATCGGGTCCCGCCAGGACCTGTACCCAGCT 300  
 Qy 93 ArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArgGly 112  
 Db 301 CGATCCCTGTGCCACACTGCGTACGCTACAGAGGCTCCCATGAGCCCGCTGGGCG 360  
 Qy 113 AsnSerGluLeuTyrHisAsnGlnThrValPheTyrArgArgProCysHisGlyGlu 132  
 Db 361 AACTCCGTCCTCCACTTACCAACACAGAGCGGTCTTCTACCGCGCGCCATGCCATGGTGAG 420  
 Qy 133 LysGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyrArgValSerLeuAlaCys 152  
 Db 421 GAAGGTACCATCCGCGCTACTGCTTGGAGCGCAGGCTCTACCGAGTCTCCCTGGCTGT 480  
 Qy 153 ValCysValArgProArgValMet 160  
 Db 481 CTGTGTGTGCGGCGCCCGGTCATG 504

RESULT 12

ABA02394

ID ABA02394 standard; DNA; 985 BP.

XX ABA02394;

AC XX 26-FEB-2002 (first entry)

DT XX Murine interleukin 174 (IL-174)-encoding DNA.

DE XX Mouse; murine; interleukin 174; IL-174; cytokine; Th2 response;

KW

KW innate immune response; inflammation; gut cell growth;  
 KW extramedullary hematopoiesis; antibody response; granuloma formation;  
 KW autoimmune condition; multiple sclerosis; systemic lupus erythematosus;  
 KW rheumatoid arthritis; diabetes; psoriasis; infectious agent;  
 KW inflammatory condition; Crohn's disease; ulcerative colitis;  
 KW pancreatitis; hepatitis; allergy; Th2-mediated condition;  
 KW systemic anaphylactic response; skin hypersensitivity response;  
 KW dermatitis; asthma; fibrosis; eosinophilic gastritis; immunomodulator;  
 KW antiinflammatory; antiarthritic; antidiabetic; antifungal;  
 KW dermatological; neuroprotective; antiallergic; agonist; antagonist; ds.  
 XX Mus sp.  
 XX Location/Qualifiers  
 FH Key 1..510  
 FT CDS /\*tag= a  
 FT /\*product= "Murine IL-174"  
 FT sig\_peptide 1..48  
 FT /\*tag= b  
 FT mat\_peptide 49..507  
 FT /\*tag= c  
 FT /\*product= "Mature murine IL-174"  
 XX WO200179288-A2.

PN 25-OCT-2001.

XX 17-APR-2001; 2001WO-US12493.

XX 18-APR-2000; 2000US-198488P.

XX (SCHE ) SCHERING CORP.

PI Hurst SD, Zurawski SM, Rennick DM;

XX WPI; 2002-034343/04.

DR P-P5DB; AAM52692.

XX Administering an interleukin 174 agonist or antagonist to a mammal  
 PT regulates various immune and inflammatory responses and is useful to  
 PT treat for example autoimmune diseases, allergies or response to an  
 PT infection  
 XX Disclosure; Page 28-29; 29pp; English.  
 PS The invention relates to methods of directing an immune response in a  
 CC mammal by the administration of an agonist or antagonist of the cytokine  
 CC interleukin 174 (IL-174). Administration of an IL-174 agonist directs the  
 CC immune response towards a Th2 response, stimulates an innate immune  
 CC response, augments the inflammatory response from epithelial or  
 CC fibroblast cells, induces gut cell growth, promotes extramedullary  
 CC haematopoiesis, or augments an antibody response in serum and faecal  
 CC material, while administration of an IL-174 antagonist directs the immune  
 CC response away from a Th2 type response, and prevents inflammation or  
 CC granuloma formation. IL-174 agonists may be used to treat autoimmune  
 CC conditions (particularly multiple sclerosis, systemic lupus  
 CC erythematosus, rheumatoid arthritis, diabetes or psoriasis), a response  
 CC to an infectious agent, or inflammatory conditions such as Crohn's  
 CC disease, ulcerative colitis, pancreatitis, or hepatitis. IL-174  
 CC antagonists may be used to treat inflammatory, allergic or Th2-mediated  
 CC conditions (e.g., systemic anaphylactic response, skin hypersensitivity  
 CC response, dermatitis, asthma, fibrosis, or eosinophilic gastritis). The  
 CC present sequence represents DNA encoding murine IL-174.

XX SQ Sequence 985 BP; 199 A; 296 C; 268 G; 222 T; 0 other;

Alignment Scores:

Pred. No.: 1.55e-55 Length: 985

Score: 709.00 Matches: 129

Percent Similarity: 82.14% Conservative: 9

Best Local Similarity: 76.79% Mismatches: 22

Query Match: 77.91% Indels: 8

DB: 21 Gaps: 1

31-JAN-2002.

21-JUN-2001; 2001WO-US19861.

22-JUN-2000; 2000US-213125P.

02-FEB-2001; 2001US-266159P.

16-MAR-2001; 2001US-0810384.

(AMGE-) AMGEN INC.

Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HO, Jing S;  
WPI; 2002-155217/20.  
P-PSDB: AAE18121.

Nucleic acid molecules encoding Interleukin 17 (IL-17) - like polypeptides useful in the treatment, prevention and diagnosis of diseases e.g. cancer

Claim 1; Fig 2; 242pp; English.

The invention relates to nucleic acid molecules encoding Interleukin 17 (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels of IL-17 protein in an animal. The IL-17 protein is useful for treating, preventing or ameliorating a disease, such as immune system dysfunction (rheumatoid arthritis, osteoarthritis, inflammatory joint disease); autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel disease, transplant rejection, graft vs. host disease); infections (HIV, hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia, sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy, atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma, leukaemia); reproductive (infertility, miscarriage, endometriosis); eye (blindness, retinal neuropathy) and treatment of diseases involving inflammation. The present sequence is mouse interleukin-17 like (IL-17L) cDNA.

Sequence 1013 BP; 227 A; 297 C; 268 G; 221 T; 0 other;

Alignment Scores:

| Pred. No.:             | 1,61e-55 | Length:       | 1013 |
|------------------------|----------|---------------|------|
| Score:                 | 709.00   | Matches:      | 129  |
| Percent Similarity:    | 82.14%   | Conservative: | 9    |
| Best Local Similarity: | 76.79%   | Mismatches:   | 22   |
| Query Match:           | 77.91%   | Indels:       | 8    |
| DB:                    | 24       | Gaps:         | 1    |

US-10-037-591A-2 (1-161) x AAD28772 (1-1013)

Qy 1 MetTyrGlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyr----- 17

Db 1 ATGTACCAGGCTGTGTGCATTCTTGCAATGATCGTGGGAACCCACCGTCAGCTTGGCG 60

Qy 18 -----SerHisTrpProSerCysCysProSerTyrsglyGlnAspThrSer 32

Db 61 ATCCAGGAGGGCTGCAGTCACCTGTGCCAGCTCTGCCCCAGCAAGACGAACCCCG 120

Qy 33 GluGluLeuLeuArgTyrPsrThrValProValProProLeuGluProAlaArgProAsn 52

Db 121 GAGGAGTGGCTGAAGTGGAGCTCTGCATCTGTGTCCCCCAGAGGCTCTGAGCCACACC 180

Qy 53 ArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIleSer 72

Db 181 CACCACGCAGAAATCTCGAGGCCACGAGGATGCGCCCTCAACAGCAGGGCCATCTCT 240

Qy 73 ProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrHisAla 92

Db 241 CTTGGAGCTATAGTGTGACAGGACTTGAAATCGGGTCTCCACGACCTGTACACAGCT 300

Qy 93 ArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArgGly 112



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Db 301 CGATGCGTGTGCCACACTGCGTACAGCTACAGACAGGCTCCACATGAGCCGCTGGC 360
QY 113 AsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArgProCysHisGlyGlu 132
Db 361 AACTCCGTCCTCCACTTACACACAGAGGCTCTTACCGGGGCCATGCCATGGCGAG 420
QY 133 LysGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyrArgValSerLeuAlaCys 152
Db 421 GAAGGTACCCATCCGCTACTGCTTGGAGCGCAGGCTCTTACCGAGTCTCCTTGGCTGT 480

QY 153 ValCysValArgProArgValMet 160
Db 481 GTGTGTGTGCGGCCCGGGTCATG 504

RESULT 14
AAD28773
ID AAD28773 standard; cDNA; 1496 BP.
XX AC
XX AAD28773;
XX 07-MAY-2002 (first entry)
XX DE Mouse non-secreted form of Interleukin-17 like (IL-17L) cDNA.
XX KW Mouse; interleukin-17 like; IL-17L; immune system dysfunction; diabetes;
KW cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;
KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;
KW autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;
KW infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;
KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;
KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;
KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;
KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;
KW cancer; ss.
XX OS Mus musculus.
XX FH Key
XX FT Location/Qualifiers
XX FT 511..993
XX FT /*tag= a
XX FT /product= "Mouse non-secreted form of IL-17L protein"
XX PN
XX PD
XX PP 21-JUN-2001; 2001WO-US19861.
XX PR 22-JUN-2000; 2000US-213125P.
XX PR 02-FEB-2001; 2001US-266159P.
XX PR 16-MAR-2001; 2001US-0810384.
XX PA (AMGE-) AMGEN INC.
XX PI Medlock E, Yeh R, Silbiger SM, Elliott GS, Nguyen HQ, Jing S;
XX WPI: 2002-155217/20.
XX P-PSDB: AAE18122.
XX PT Nucleic acid molecules encoding Interleukin 17 (IL-17) - like
XX PT polypeptides useful in the treatment, prevention and diagnosis of
XX PT diseases e.g. cancer -
XX PS Claim 1; Fig 2; 242pp; English.
XX The invention relates to nucleic acid molecules encoding Interleukin 17
XX (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels
XX of IL-17 protein in an animal. The IL-17 protein is useful for treating,
XX preventing or ameliorating a disease, such as immune system dysfunction
XX (rheumatoid arthritis, osteoarthritis, inflammatory joint disease);
XX autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel
XX disease, transplant rejection, graft vs. host disease); infections (HIV,

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CC (hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,
CC sepsis); respiratory dysfunction (Alzheimer's, Parkinson's disease); lung
CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin
CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone
CC (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy
CC atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma
CC leukaemia); reproductive (infertility, miscarriage, endometriosis), eye
CC (blindness, retinal neuropathy) and treatment of diseases involving
CC inflammation. The present sequence is non-secreted form of mouse
CC Interleukin-17 like (IL-17L) cDNA.
XX SQ Sequence 1496 BP; 347 A; 417 C; 410 G; 322 T; 0 other;

Alignment Scores:
Pred. No.: 7.6e-54 Length: 1496
Score: 693.00 Matches: 126
Percent Similarity: 81.93% Conservative: 10
Best Local Similarity: 75.90% Mismatches: 22
Query Match: 76.15% Indels: 8
DB: 24 Gaps: 1

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US-10-037-591A-2 (1-161) x AAD28773 (1-1496)

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QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyr----- 17
Db 490 AAGGCTGTGTCATCTTGGCAATGATCGTGGGAACCCACACCGTCAGCTTGGCGATCCAG 549
QY 18 -----SerHisTrpProSerCysCysProSerLysGlyGlnAspThrSerGluGlu 34
Db 550 GAGGCTCGATGCTACCTTCCCGAGCTGTCGCCACCAAGACAGAACCCCGGAGGAG 609
QY 35 LeuLeuArgTrpSerThrValProValProLeuGluProAlaArgProAsnArgHis 54
Db 610 TGGCTGAAGTGGAGCTCTGCTCTGTCGCCGCCAGAGCCTCTGAGCCACACCCACACC 659
QY 55 ProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIleSerProTrp 74
Db 670 GCAGAACTCTGCAGGGCCAGCAAGATGGCCCCCTCAACAGCAGGGCCATCTCTCTTGG 729
QY 75 ArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrHisAlaArgCys 94
Db 730 AGCTATGAGTTGGACAGGACTTGAATCGGGTCCCCCAGGACCTGTACCACGCTCCATGC 789
QY 95 LeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArgGlyAsnSer 114
Db 790 CTGTGCCACACTGCGTCAAGCTACAGACAGGCTCCACATGAGCCCGCTGGCAACTCC 849
QY 115 GluLeuLeuTyrHisAsnGlnThrValPheTyrArgArgProCysHisGlyGluLysGly 134
Db 850 GTCCCACTTTACCACACAGCAGCTTCTTACCGGGGCCATGCCATGGCGAGGAGGT 909
QY 135 ThrHisLysGlyTyrCysLeuGluArgArgLeuTyrArgValSerLeuAlaCysValCys 154
Db 910 ACCCATCCCGCTACTGCTTGGAGCGCAGGCTCTACCGAGTCTCTCTTGGCTGTGTGTGT 969

QY 155 ValArgProArgValMet 160
Db 970 GTGCGGCCCGGGTCAATG 987

RESULT 15
AAA58987
ID AAA58987 standard; cDNA; 620 BP.
XX AC
XX AAA58987;
XX 07-NOV-2000 (first entry)
XX DE cDNA encoding a murine interleukin (IL) 174 polypeptide.
XX KW Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;
XX IL-177; IL-171; cell proliferation; cancer; ss.
XX OS Mus sp.

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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| XX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| FN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| WO2000042188-A2.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| XX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| PD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 20-JUL-2000.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| XX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Pf                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 10-JAN-2000; 2000WO-US00006.                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| XX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| PR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 11-JAN-1999; 99US-0228822.                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| XX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| PA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| (SCHE ) SCHERING CORP.                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| XX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| PI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Gorman DM, Bazan JF, Kastelein RA;                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| XX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| DR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| WPI; 2000-456130/40.                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| DR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| P-PSDB; AAB07599.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| XX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| PT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| New isolated polynucleotide encoding a mammalian Interleukin-17 like protein used to identify genes for homologous proteins -                                                                                                                                                                                                                                                                                                                                                                      |
| PT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Disclosure; Page 17; lllpp; English.                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| XX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| CC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| The present sequence encodes an interleukin-174 (IL-174) polypeptide. The polypeptide is an IL-17-like (CvIA-8 related) protein. It is a member of a new group of interleukins, IL-170 polypeptides. The members comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170 protein can be used to treat abnormal proliferation e.g. cancer or degenerative conditions. Antibodies can be used in diagnostic methods to detect over production of IL-170 protein in cells or body fluids. |
| CC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Sequence 620 BP; 125 A; 183 C; 188 G; 124 T; 0 other;                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| XX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| SQ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Alignment Scores:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| Pred. No.:                 4.45e-36          Length:              620                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Score:                    493.00           Matches:              100                                                                                                                                                                                                                                                                                                                                                                                                                               |
| Percent Similarity:      84.25%           Conservative:          7                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Best Local Similarity:   78.74%           Mismatches:          20                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| Query Match:             54.18%           Indels:                3                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| DB:                        21                Gaps:                  0                                                                                                                                                                                                                                                                                                                                                                                                                              |
| US-10-037-591A-2 (1-161) x AAAS8987 (1-620)                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 34 GluLeuLeuArgTrpSerThrValProValProLeuGluProAlaArgProAsnArg 53<br>    :    :   :::                                                                                                                                                                                                                                                                                                                                                                                                                |
| Dd                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 26 GAGTGGCTGAAGTGAGGTGCATCTGTATCCCCCGACAGGCCCTTCAGCACACCAC 85                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 54 HisProGluSerCysArgAlaSerGluaspGlyProLeuAsnSerArgAlaIleSerPro 73<br>         :       :                                                                                                                                                                                                                                                                                                                                                                                                           |
| Dd                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 86 CACGCAGAATCTCGAGGGCCAGCAAGGATTG-CCTCTAACACAGCGGCCCATCTCTCT 144<br>         :       :                                                                                                                                                                                                                                                                                                                                                                                                            |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 74 TrpArgTyrrGlutLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrrHisAlaArg 93<br>         :       :                                                                                                                                                                                                                                                                                                                                                                                                        |
| Dd                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 145 TGGAGCTATGATTTGGACAGGACTTGAAATCGGGTCCCACAGGACTGGTACCACGCYCGA 204<br>         :       :                                                                                                                                                                                                                                                                                                                                                                                                         |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 94 CysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProrAggLYasn 113<br>         :       :                                                                                                                                                                                                                                                                                                                                                                                                          |
| Dd                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 205 TGCTGTGCCACACTCGGTCCAGCTACAGACAGGCTCCACATGGACCCCTGGGCAAC 264<br>         :       :                                                                                                                                                                                                                                                                                                                                                                                                             |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 114 SerCluLeuLeuTyrrHisAsnGlnThrValPhetYrrargProCysHisGLylLlys 133<br>         :       :                                                                                                                                                                                                                                                                                                                                                                                                           |
| Dd                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 265 TCCTGCCACTTTACCACAACACAGACGGTCTTCTTACC GGCGGCATGCAT-GGCGAGGAA 323<br>         :       :                                                                                                                                                                                                                                                                                                                                                                                                        |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 134 GlyThrHisLysGlyTYrrCysLeuGluArgLeutyrrGValSerLeuAlaCysVal 153<br>         :       :                                                                                                                                                                                                                                                                                                                                                                                                            |
| Dd                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 324 GFPACCATCGCCCTACTGCTTGAGCGCAGGTC-TACCGAGHCTCTTGGCTTGtGTG 382<br>         :       :                                                                                                                                                                                                                                                                                                                                                                                                             |
| Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 154 CysValArgProArgValMet 160                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| Dd                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 383 TGTGTGGCGGCCCGGGTCA 403                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |

Search completed: May 12, 2003, 02:05:54  
Job time : 166 secs

GenCore version 5.1.4.p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2003, 00:33:18 ; Search time 163 Seconds  
(without alignments)  
8897.466 Million cell updates/sec

Title: US-10-037-591A-1

Perfect score: 644

Sequence: 1 ctcaagtcactccctcaaaaa.....ggccccgtgtgatggctag 644

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_101002.\*

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1: /SID52/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SID52/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SID52/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SID52/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SID52/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SID52/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SID52/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SID52/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SID52/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SID52/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SID52/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SID52/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SID52/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SID52/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SID52/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SID52/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                   |
|------------|-------|-------------|--------|----|-------------------------------|
| 1          | 644   | 100.0       | 644    | 24 | AAD28771 Human Interleukin-   |
| 2          | 644   | 100.0       | 644    | 24 | ABA03213 Human IL-17 receptor |
| 3          | 493   | 76.6        | 504    | 21 | AAAS8986 cDNA encoding a hu   |
| 4          | 493   | 76.6        | 504    | 21 | AAAS9158 Human Interleukin    |
| 5          | 493   | 76.6        | 504    | 21 | ABA02393 Human cDNA encodin   |
| 6          | 478.4 | 74.3        | 1320   | 22 | AAAS09511 Native sequence of  |
| 7          | 478.4 | 74.3        | 1320   | 22 | AAC85969 Human PRO10272 cDN   |
| 8          | 478.4 | 74.3        | 1320   | 22 | AAF92135 DNA encoding novel   |
| 9          | 418.2 | 64.9        | 1355   | 23 | AAAS9559                      |

|    |       |      |       |    |           |                    |
|----|-------|------|-------|----|-----------|--------------------|
| 10 | 336.8 | 52.3 | 1013  | 24 | AAD28772  | Mouse Interleukin- |
| 11 | 336.2 | 52.2 | 1496  | 24 | AAD28773  | Mouse non-secreted |
| 12 | 335.2 | 52.0 | 985   | 21 | AAAS8986  | cDNA encoding a mu |
| 13 | 335.2 | 52.0 | 985   | 21 | AAAS9160  | Murine interleukin |
| 14 | 335.2 | 52.0 | 985   | 24 | ABA02394  | cDNA encoding a mu |
| 15 | 249.6 | 38.8 | 620   | 21 | AAAS8987  | cDNA encoding a mu |
| 16 | 249.6 | 38.8 | 620   | 21 | AAAS9159  | Nucleotide sequenc |
| 17 | 55.4  | 8.6  | 1067  | 21 | AAZ36836  | Human interleukin  |
| 18 | 55.4  | 8.6  | 1067  | 23 | AA167878  | Human interleukin- |
| 19 | 53.8  | 8.4  | 591   | 21 | AAA09153  | Human LP-48 gene.  |
| 20 | 53.8  | 8.4  | 591   | 24 | AAD38083  | cDNA encoding a no |
| 21 | 53.8  | 8.4  | 1047  | 21 | AAZ29728  | Human Interleukin  |
| 22 | 53.8  | 8.4  | 1047  | 22 | AAZ29728  | Human DNA encoding |
| 23 | 53.8  | 8.4  | 1047  | 22 | AAZ29728  | Human cDNA encodin |
| 24 | 53.8  | 8.4  | 1107  | 21 | AAAS8991  | cDNA encoding a hu |
| 25 | 53.8  | 8.4  | 1107  | 21 | AAAS8991  | cDNA encoding a hu |
| 26 | 53.8  | 8.4  | 1177  | 22 | AAD15291  | Human Interleukin  |
| 27 | 53.8  | 8.4  | 1177  | 22 | AAD15291  | Human IL-17E hybri |
| 28 | 45    | 7.0  | 45    | 22 | AAAS09523 | Gene encoding a su |
| 29 | 42    | 6.5  | 10732 | 21 | AAAL0594  | Human interleukin- |
| 30 | 41.4  | 6.4  | 540   | 20 | AAZ89401  | cDNA encoding a hu |
| 31 | 41.4  | 6.4  | 543   | 21 | AAAS8980  | cDNA encoding a hu |
| 32 | 41.4  | 6.4  | 543   | 21 | AAAS9152  | Human PRO1031 nucl |
| 33 | 41.4  | 6.4  | 687   | 20 | AAZ34282  | Human PRO1031 (UNO |
| 34 | 41.4  | 6.4  | 687   | 21 | AAZ78577  | cDNA clone DNA5929 |
| 35 | 41.4  | 6.4  | 687   | 21 | AAZ75694  | Human PRO1031 prot |
| 36 | 41.4  | 6.4  | 687   | 21 | AAZ58608  | Human Interleukin  |
| 37 | 41.4  | 6.4  | 687   | 21 | AAZ29727  | Human cDNA encodin |
| 38 | 41.4  | 6.4  | 687   | 22 | AAAS09509 | Human cDNA sequenc |
| 39 | 41.4  | 6.4  | 687   | 22 | AAZ21466  | Human PRO1031 cDNA |
| 40 | 41.4  | 6.4  | 687   | 22 | AAZ21466  | Human PRO1031 codi |
| 41 | 41.4  | 6.4  | 687   | 22 | AAZ21466  | Human PRO1031 codi |
| 42 | 41.4  | 6.4  | 689   | 21 | AAZ95780  | Human immune syste |
| 43 | 41.4  | 6.4  | 704   | 22 | AAH79235  | Human cell factor- |
| 44 | 41.4  | 6.4  | 705   | 20 | AAZ15870  | cDNA encoding inte |
| 45 | 41.4  | 6.4  | 705   | 21 | AAZ75787  | DNA encoding a hum |

#### ALIGNMENTS

RESULT 1

AAD28771

ID AAD28771 standard; cDNA; 644 BP.

XX AAD28771;

AC AAD28771;

XX 07-MAY-2002 (first entry)

DE Human Interleukin-17 like (IL-17L) cDNA.

Human; interleukin-17 like; IL-17L; immune system dysfunction; diabetes; cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus; inflammatory bowel disease; neuronal dysfunction; transplant rejection; autoimmune disorder; lung; skin; kidney; bone; eye; vascular system; infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis; cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema; eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease; epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis; leukaemia; retinal neuropathy; infertility; miscarriage; inflammation; cancer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 159..644

FT /tag- a

FT /product= "Human IL-17L protein"

FT sig\_peptide 159..206

FT /tag- b

FT mat\_peptide 207..641

FT /tag- c

FT /product= "Mature IL-17L protein"



CC coding sequences are useful for treating a pathological condition related  
CC to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g.  
CC viral infections), weight disorders (e.g. obesity), neuronal dysfunction  
CC disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin  
CC disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis),  
CC bone disease (e.g. osteoporosis), vascular system disorders (e.g.  
CC ischaemia), eye disorders, reproductive disorders, tumours and  
CC inflammation. The present sequence is the coding sequence for IL-17E, a  
CC human IL-17 receptor like protein ligand.

Sequence 644 BP; 144 A; 204 C; 173 G; 123 T; 0 other;

|                       |                 |                   |           |             |
|-----------------------|-----------------|-------------------|-----------|-------------|
| Query Match           | 100.0%;         | Score 644;        | DB 24;    | Length 644; |
| Best Local Similarity | 100.0%;         | Pred. NO. 2e-164; |           |             |
| Matches 644;          | Conservative 0; | Mismatches 0;     | Indels 0; |             |

|    |     |                                                                    |     |
|----|-----|--------------------------------------------------------------------|-----|
| QY | 1   | CTCAAGTCACTCCCTCTAAAAAGACAGTGGAAATAAATTTGAATAAACAACAGGCTTGCT       | 60  |
| Db | 1   | CTCAAGTCACTCCCTCTAAAAAGACAGTGGAAATAAATTTGAATAAACAACAGGCTTGCT       | 60  |
| QY | 61  | GAAATAAAATCAGGACTCCCTAACCTGCTCCAGCTCAGCCTGCTTCACAGAGGCTTGCTGAC     | 120 |
| Db | 61  | GAAATAAAATCAGGACTCCCTAACCTGCTCCAGCTCAGCCTGCTTCACAGAGGCTTGCTGAC     | 120 |
| QY | 121 | TCAGTGGCCCCACTTTGTGACTGAGTGTGACGTGCCAGCCAGCAGTGTACCAAGTGGTTGCAATCT | 180 |
| Db | 121 | TCAGTGGCCCCACTTTGTGACTGAGTGTGACGTGCCAGCCAGCAGTGTACCAAGTGGTTGCAATCT | 180 |
| QY | 181 | TGGCAATTTGGTCATGGGAACCCACACCTACAGCCACATGTGGCCAGCTGCTGCCCCAGCAAG    | 240 |
| Db | 181 | TGGCAATTTGGTCATGGGAACCCACACCTACAGCCACATGTGGCCAGCTGCTGCCCCAGCAAG    | 240 |
| QY | 241 | GGCAGGACACCTCTGAGGAGCTGCTGAGGTGTGAGCAGTGTGCCCTGTGCTCCCTTAGAGC      | 300 |
| Db | 241 | GGCAGGACACCTCTGAGGAGCTGCTGAGGTGTGAGCAGTGTGCCCTGTGCTCCCTTAGAGC      | 300 |
| QY | 301 | CTGCTAGGCCCAACCCGCCACCCAGAGTCTGTGTAGGGCCAGTGAAGATGACACCCCTCAACA    | 360 |
| Db | 301 | CTGCTAGGCCCAACCCGCCACCCAGAGTCTGTGTAGGGCCAGTGAAGATGACACCCCTCAACA    | 360 |
| QY | 361 | GCAGGGCCATCTCCCTCTGGAGATATGAGTTGACAGAGACTGTGACCCGGCTCCCCCGAG       | 420 |
| Db | 361 | GCAGGGCCATCTCCCTCTGGAGATATGAGTTGACAGAGACTGTGACCCGGCTCCCCCGAG       | 420 |
| QY | 421 | ACCTGTACCACGCCCGCTTGCTCTGTGCCCGACCTCGCTCAGCCCTACAGACAGGCTCCACCA    | 480 |
| Db | 421 | ACCTGTACCACGCCCGCTTGCTCTGTGCCCGACCTCGCTCAGCCCTACAGACAGGCTCCACCA    | 480 |
| QY | 481 | TGNACCCCGGGGCAACTCGGAGCTGCTTACCAACAACAGAGTGTCTTCTACCGGCGGC         | 540 |
| Db | 481 | TGNACCCCGGGGCAACTCGGAGCTGCTTACCAACAACAGAGTGTCTTCTACCGGCGGC         | 540 |
| QY | 541 | CATGCCATGGCGAGAGGGGACCCACAAGGGCTACTGCTTGGAGCGCAGGCTGTACCCG         | 600 |
| Db | 541 | CATGCCATGGCGAGAGGGGACCCACAAGGGCTACTGCTTGGAGCGCAGGCTGTACCCG         | 600 |
| QY | 601 | TTTCTTTAGCTTGTGTGTGTGTGCGGCCCGCGTGTGTATGGGCTAG                     | 644 |
| Db | 601 | TTTCTTTAGCTTGTGTGTGTGTGCGGCCCGCGTGTGTATGGGCTAG                     | 644 |

### RESULT 3

AAA58986

ID AAA58986 standard; cDNA; 504 BP.

AA  
AC  
AAA58986:AC  
XX  
AAA58986;

DT 07-NOV-20

XX  
0007-NOV-10 (first entry)

DE CDNA encoding a human interleukin (IL) 174 polypeptide.

XX cDNA encoding a human interleukin (IL) 1/4 polypeptide.  
KW Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;  
KW IL-177; IL-171; cell proliferation; cancer; ss.

|          |                                                                          |                                                          |     |
|----------|--------------------------------------------------------------------------|----------------------------------------------------------|-----|
| Db       | 360                                                                      | GGAGCTGCTTCTACCAACAGACTGTCTTCTACCGCGGCCATGCCATGCGAGAAAGG | 419 |
| QY       | 560                                                                      | CACCCACAAGGCTACTGCTGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTG   | 619 |
| Db       | 420                                                                      | CACCCACAAGGCTACTGCTGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTG   | 479 |
| QY       | 620                                                                      | TGTGCGGCCCCGTGTGATGGGCTAG                                | 644 |
| Db       | 480                                                                      | TGTGCGGCCCCGTGTGATGGGCTAG                                | 504 |
| RESULT 4 |                                                                          |                                                          |     |
| AAA59158 |                                                                          |                                                          |     |
| ID       | AAA59158 standard; cDNA; 504 BP.                                         |                                                          |     |
| XX       | XX                                                                       |                                                          |     |
| XX       | AAA59158;                                                                |                                                          |     |
| XX       | XX                                                                       |                                                          |     |
| DT       | 07-NOV-2000 (first entry)                                                |                                                          |     |
| DE       | XX                                                                       |                                                          |     |
| DE       | cDNA encoding a human interleukin-174 polypeptide.                       |                                                          |     |
| XX       | XX                                                                       |                                                          |     |
| KW       | Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;    |                                                          |     |
| KW       | IL-174; IL-176; IL-177; cell proliferation; cancer; ss.                  |                                                          |     |
| XX       | XX                                                                       |                                                          |     |
| OS       | Homo sapiens.                                                            |                                                          |     |
| XX       | XX                                                                       |                                                          |     |
| Key      | Location/Qualifiers                                                      |                                                          |     |
| FT       | 19..504                                                                  |                                                          |     |
| FT       | CDS                                                                      |                                                          |     |
| FT       | /tag- a                                                                  |                                                          |     |
| FT       | /product= "interleukin-174"                                              |                                                          |     |
| FT       | 19..66                                                                   |                                                          |     |
| FT       | sig_peptide                                                              |                                                          |     |
| FT       | /tag- b                                                                  |                                                          |     |
| FT       | 67..501                                                                  |                                                          |     |
| FT       | mat_peptide                                                              |                                                          |     |
| FT       | /tag- c                                                                  |                                                          |     |
| XX       | XX                                                                       |                                                          |     |
| PN       | WO200042187-A1.                                                          |                                                          |     |
| XX       | XX                                                                       |                                                          |     |
| PD       | 20-JUL-2000.                                                             |                                                          |     |
| XX       | XX                                                                       |                                                          |     |
| PF       | 10-JAN-2000; 2000WO-US00005.                                             |                                                          |     |
| XX       | XX                                                                       |                                                          |     |
| PR       | 11-JAN-1999; 99US-0229402.                                               |                                                          |     |
| XX       | XX                                                                       |                                                          |     |
| PA       | (SCHE ) SCHERING CORP.                                                   |                                                          |     |
| XX       | XX                                                                       |                                                          |     |
| PI       | Gorman DM, Bazan JF, Kastelein RA;                                       |                                                          |     |
| PI       | XX                                                                       |                                                          |     |
| DR       | WPI; 2000-476060/41.                                                     |                                                          |     |
| DR       | P-PSDB; AAB07692.                                                        |                                                          |     |
| XX       | XX                                                                       |                                                          |     |
| FT       | New DNA sequence encoding a mammalian homolog of CTLA-8, designated      |                                                          |     |
| FT       | interleukin-171 (IL-171), useful for recombinant production of IL-171    |                                                          |     |
| FT       | which can be used for treating conditions associated with abnormal       |                                                          |     |
| FT       | physiology or development -                                              |                                                          |     |
| XX       | XX                                                                       |                                                          |     |
| PS       | Disclosure; Page 19; 111pp; English.                                     |                                                          |     |
| XX       | XX                                                                       |                                                          |     |
| CC       | The present sequence encodes an interleukin (IL)-174 polypeptide.        |                                                          |     |
| CC       | It is a mammalian homologue of the cytokine designated CTLA-8 (also      |                                                          |     |
| CC       | referred to as IL-17). The specification also describes homologues       |                                                          |     |
| CC       | IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA      |                                                          |     |
| CC       | sequence encoding IL-171 is useful for identifying genes, mRNA and       |                                                          |     |
| CC       | cDNA molecules which code for related or homologous proteins. The        |                                                          |     |
| CC       | IL-171 protein, antibodies against IL-171, and compounds which have      |                                                          |     |
| CC       | binding affinity to IL-171 are useful in treatment of conditions         |                                                          |     |
| CC       | associated with abnormal physiology or development, including abnormal   |                                                          |     |
| CC       | proliferation, e.g. cancerous conditions, or degenerative conditions.    |                                                          |     |
| CC       | The IL-171 protein can be used in kits and assay methods for identifying |                                                          |     |
| CC       | compounds that selectively bind to IL-171.                               |                                                          |     |
| XX       | XX                                                                       |                                                          |     |
| SQ       | Sequence 504 BP; 98 A; 165 C; 148 G; 93 T; 0 other;                      |                                                          |     |

Query Match

76.6%; Score 493; DB 21; Length 504;

Query Match 76.6%; Score 493; DB 21; Length 504;

|          |                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |              |               |            |    |        |
|----------|-----------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------|---------------|------------|----|--------|
|          | Best Local Similarity | 99.8%;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Pred.        | No..1.4e-123; |            |    |        |
|          | Matches               | 504;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Conservative | 0;            | Mismatches | 0; | Indels |
| QY       | 140                   | TGAGTGTGCAGTGCCCGCAGCATGTACCAAGTGGTTGCATCTTTGGCAATGG1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |              |               |            |    |        |
| Db       | 1                     | TGAGTGTGCAGTG-CCAGCATGTACCAGGTGTTGCATTCTTTGGCAATG1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |              |               |            |    |        |
| QY       | 200                   | CCACACCTACAGCCACTGGCCAGTGCTGCCCCCAGCAAAGGCGAGCACAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |              |               |            |    |        |
| Db       | 60                    | CCACACCTACAGCCACTGGCCAGTGCTGCCCCCAGCAAAGGCGAGCACAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |              |               |            |    |        |
| QY       | 260                   | GCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCTTAGAGCCTGTCTAGGCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |              |               |            |    |        |
| Db       | 120                   | GCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCTTAGAGCCTGTCTAGGCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |              |               |            |    |        |
| QY       | 320                   | CCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGCGCCAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |              |               |            |    |        |
| Db       | 180                   | CCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGCGCCAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |              |               |            |    |        |
| QY       | 380                   | GAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGACCTGTACCA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |              |               |            |    |        |
| Db       | 240                   | GAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGACCTGTACCA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |              |               |            |    |        |
| QY       | 440                   | CCTGTGCCCGGCACTCGGTCAGCCTACAGACAGGCTCCACATCGACCCCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |              |               |            |    |        |
| Db       | 300                   | CCTGTGCCCGGCACTCGGTCAGCCTACAGACAGGCTCCACATCGACCCCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |              |               |            |    |        |
| QY       | 500                   | GGAGTGTCTTACCAACAACAGACAGTCTTCTTACC GGCGGCCCATGCCATGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |              |               |            |    |        |
| Db       | 360                   | GGAGTGTCTTACCAACAACAGACAGTCTTCTTACC GGCGGCCCATGCCATGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |              |               |            |    |        |
| QY       | 560                   | CACCCACAAGGGCTACTGCTGGAGCGCAGGCTGTACCGTGTTCCTTAGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |              |               |            |    |        |
| Db       | 420                   | CACCCACAAGGGCTACTGCTGGAGCGCAGGCTGTACCGTGTTCCTTAGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |              |               |            |    |        |
| QY       | 620                   | TGTGCGGGCCCGTGTGATGGGCTAG 644                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |              |               |            |    |        |
| Db       | 480                   | TGTGCGGGCCCGTGTGATGGGCTAG 504                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |              |               |            |    |        |
| RESULT   | 5                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |              |               |            |    |        |
| ABA02393 | ID                    | ABA02393 standard; DNA; 504 BP.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |              |               |            |    |        |
| XX       | AC                    | ABA02393;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |              |               |            |    |        |
| XX       | DT                    | 26-FEB-2002 (first entry)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |              |               |            |    |        |
| XX       | DE                    | Human interleukin 174 (IL-174)-encoding DNA.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |              |               |            |    |        |
| KW       | XX                    | Human; interleukin 174; IL-174; cytokine; Th2 response; innate immune response; inflammation; antibody response; granulomatous disease; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; Crohn's disease; ulcerative colitis; inflammatory condition; allergy; Th2-mediated conditions; pancreatic adenocarcinoma; skin hypersensitivity reactions; dermatitis; asthma; fibrosis; eosinophilic gastritis; intestinal inflammation; antiarthritic; antidiabetic; antifungal; dermatological; neuroprotective; antiallergic; agonist; OS |              |               |            |    |        |
| XX       | OS                    | Homo sapiens.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |              |               |            |    |        |
| XX       | Key                   | Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |              |               |            |    |        |
| PH       | FT                    | 19..504                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |              |               |            |    |        |
| FT       | FT                    | /tag= a                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |              |               |            |    |        |
| FT       | FT                    | /product= "Human IL-174"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |              |               |            |    |        |
| FT       | FT                    | 19..66                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |              |               |            |    |        |
| FT       | FT                    | /tag= b                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |              |               |            |    |        |
| FT       | FT                    | 67..501                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |              |               |            |    |        |
| FT       | FT                    | /tag= c                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |              |               |            |    |        |
| FT       | FT                    | /product= "Mature human IL-174"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |              |               |            |    |        |









RESULT 9

AA593559  
ID AA593559 standard; cDNA; 1355 BP.  
XX  
AC AA593559;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE DNA encoding novel human diagnostic protein #29363.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
XX  
PR 23-AUG-2000; 2000US-0649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
XX Drmanac RT, Liu C, Tang YT;  
PI  
PI  
DR WPI: 2001-639362/73.  
DR P-PSDB; ABG29372.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity  
XX  
PS Claim 1; SEQ ID No 29363; 103pp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AA564197-AA594564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 1355 BP; 277 A; 421 C; 383 G; 274 T; 0 other;  
Query Match 64.9%; Score 418.2; DB 23; Length 1355;  
Best Local Similarity 94.4%; Pred. No. 3.5e-103;  
Matches 454; Conservative 0; Mismatches 3; Indels 24; Gaps 1;  
QY 167 GGTGGTTCATCTTGGCAATGGTCATGGGAACCCACACCTACAGCACTGGCCAGCTG 226  
DB 84 GGTGGTTCATCTTGGCAATGGTCATGGGAACCCACACCTACAGCACTGGCCAGCTG 143  
QY 227 CTGCCCCAGCAAGGCGAGCACCTCTGAGGAGCTGTGAGGTGGAGCACTGTGCTGT 286  
|||||

Db 144 CTGCCCCAGCAAGGCGAGCACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCTGT 203  
QY 287 GCCTCCCTAGAGCCTGTAGGCCCAACCCACCCAGAGTCTCTGTAGGCCAGTGAAGA 346  
Db 204 GCCTCCCTAGAGCCTGTAGGCCCAACCCACCCAGAGTCTCTGTAGGCCAGTGAAGA 263  
QY 347 TGGACCCCTCAACAGCAGGCGCATCTCCCTCTGGAGATATGA----- 388  
Db 264 TGGACCCCTCAACAGCAGGCGCATCTCCCTCTGGAGATATGAGCCTGACAGTCCGCC 323  
QY 389 -----GTTGGACAGAGACTTGAACCGGCTCCCGGAGGAGCTGTACCAAGCCGCTTGCCT 442  
Db 324 CCACAGGTTGGACAGAGACTTGAACCGGCTCCCGGAGGAGCTGTACCAAGCCGCTTGCCT 383  
QY 443 GTGCCGCACTGCTGCTAGCCTACAGAGAGCTCCACATGACACCCCGGGGCACTCGGA 502  
Db 384 GTGCCGCACTGCTGCTAGCCTACAGAGAGCTCCACATGACACCCCGGGGCACTCGGA 443  
QY 503 GCTGCTCTACCAACAGAGACTCTCTTCTACCGGCGGCGCATGCCATGGCAGAGGGCAC 562  
Db 444 GCTGCTCTACCAACAGAGACTCTCTTCTACCGGCGGCGCATGCCATGGCAGAGGGCAC 503  
QY 563 CCACAGGCGCTACTGCTGTGAGCGCAGGCTGTACCGGCTTTCTTCTTACGCTGTGTGTGTGT 622  
Db 504 CCACAGGCGCTACTGCTGTGAGCGCAGGCTGTACCGGCTTTCTTCTTACGCTGTGTGTGTGT 563  
QY 623 G 623  
Db 564 G 564  
RESULT 10  
AAD28772  
ID AAD28772 standard; cDNA; 1013 BP.  
XX  
AC AAD28772;  
XX  
DT 07-MAY-2002 (first entry)  
XX  
DE Mouse Interleukin-17 like (IL-17L) cDNA.  
XX  
KW Mouse; interleukin-17 like; IL-17L; immune system dysfunction; diabetes;  
KW cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;  
KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;  
KW autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;  
KW infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;  
KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;  
KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;  
KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;  
KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;  
KW cancer; ss.  
OS Mus musculus.  
XX  
XX Key Location/Qualifiers  
FH CDS 1..510  
FT /tag= a  
FT /product= "Mouse IL-17L protein"  
FT sig\_peptide 1..53  
FT /tag= b  
FT mat\_peptide 54..507  
FT /tag= c  
FT /product= "Mature IL-17L protein"  
FT  
FT  
FT  
PN WO200208285-A2.  
XX  
XX 31-JAN-2002.  
PD  
XX 21-JUN-2001; 2001WO-US19861.  
XX  
XX 22-JUN-2000; 2000US-213125P.  
PR 02-FEB-2001; 2001US-266159P.  
PR 16-MAR-2001; 2001US-0810384.  
PR



```
Query Match      52.2%; Score 336.2; DB 24; Length 1496;
Best Local Similarity 79.1%; Pred. No. 5.7e-81;
Matches 423; Conservative 0; Mismatches 88; Indels 24; Gaps 1;

QY 134 TGTGCTAGTGTGCTGAGTCCCGCAGCATGTACAGGTGGTGTGCTATCTTGGCAATGTCAT 193
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 459 TGTGCTAAGAGTGGCTGTGTGCTACCTGGCCCAAGGCTGTGCTATCTTGGCAATGTCAT 518
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 194 GGGAAACCCACACTACAGC-----CACTGGCCCCAGCTGCTG 229
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 519 GGGAAACCCACACTACAGC-----CACTGGCCCCAGCTGCTG 578
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 230 CCCCAGCAAGGCGAGGACACCTCTGAGGAGTGTGTGAGTGAGACACTGTGCTGTGCC 289
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 579 CCCCAGCAAGGCGAGGACACCTCTGAGGAGTGTGTGAGTGAGACACTGTGCTGTGCC 638
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 290 TCCCTTAGAGCTGTAGTCCCAACCGCCACAGCTCCTGTAGGCGCACTGAGATGG 349
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 639 CCCCAGCAAGCTGTAGTCCCAACCGCCACAGCTCCTGTAGGCGCACTGAGATGG 698
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 350 ACCCTCTCAACAGCGGGCCATCTCCCTCTGGAGATATGATGGACAGACTTGAACCG 409
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 699 CCCCCTCAACAGCGGGCCATCTCTCTGGAGCTATGATGGACAGGACTTGAATCG 758
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 410 GTCCCCAGGACCTGTACACCGCGGTGCTGTGCGCGCACTGGCTCAGCCTACAGAC 469
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 759 GGTCCCCAGGACCTGTACACCGCTGATGCTGTGCCACACTGGCTCAGCCTACAGAC 818
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 470 AGGCTCCACATGGACCCCGGGGCAACTCGAGCTGCTTACCACAAACAGACTGCTT 529
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 819 AGGCTCCACATGGACCCCGGGGCAACTCGAGCTGCTTACCACAAACAGACTGCTT 878
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 530 CTACCGGCGGCGCATGCCATGGCGAGAGGCGCACCAAGGCTACTGCTGGAGCGCAG 589
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 879 CTACCGGCGGCGCATGCCATGGCGAGAGGCTACCCATCCCGCTACTGCTGGAGCGCAG 938
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 590 GGTGACCGCTGTCTTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 644
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 939 GCTCTACCGAGTCTCTTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 993
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
AAA5988
ID AAA5988 standard; cDNA; 985 BP.
XX
AC AAA58988;
XX
DT 07-NOV-2000 (first entry)
XX
DE cDNA encoding a murine interleukin (IL) 174 polypeptide.
XX
KW Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;
IL-177; IL-171; cell proliferation; cancer; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..510
FT sig_peptide 1..48 /*tag= a
FT mat_peptide 49..507 /*tag= b
FT /*tag= c
XX
PN WO200042188-A2.
XX
PD 20-JUL-2000.
XX
PF 10-JAN-2000; 2000WO-US00006.
XX
PR 11-JAN-1999; 99US-0228822.
XX
PA (SCHE ) SCHERING CORP.

Gorman DM, Bazan JF, Kastelein RA;
WPI: 2000-466130/40.
P-PSDB; AAB07600.
New isolated polynucleotide encoding a mammalian Interleukin-17 like
protein used to identify genes for homologous proteins -
Disclosure; Page 18; 11pp; English.
The present sequence encodes an interleukin-174 (IL-174) polypeptide.
The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a
member of a new group of interleukins, IL-170 polypeptides. The members
comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170
protein can be used to treat abnormal proliferation e.g. cancer
or degenerative conditions. Antibodies can be used in diagnostic
methods to detect over production of IL-170 protein in cells or body
fluids.
Sequence 985 BP; 199 A; 296 C; 268 G; 222 T; 0 other;
Query Match      52.0%; Score 335.2; DB 21; Length 985;
Best Local Similarity 81.0%; Pred. No. 9.1e-81;
Matches 413; Conservative 0; Mismatches 73; Indels 24; Gaps 1;

QY 159 ATGTACAGAGTGTGCTTGGCAATGCTGTCATGGGAACCCACACTACAGC----- 212
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 ATGTACAGAGTGTGCTTGGCAATGCTGTCATGGGAACCCACACTACAGC----- 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 213 -----CACTGGCGGAGTGTGTCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 254
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 ATCCAGGAGGCGTGCAGTCACTTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 255 GAGGAGCTGTGAGTGGAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 314
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 GAGGAGTGGCTGAAGTGGAGCTCTGCACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 315 CGCACCCAGAGTCTGTAGGCGCAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 374
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 CACCAGCAGATCCTGCAGGCGCAGCAGGATGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 375 CCCTGGAGATATGAGTGGACAGAGCTTGAACGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 CCTTGGAGCTATGAGTGGACAGGACTTGAATCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 435 CGTTGCTGTGCGCGCAGCTGCTACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 494
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 301 CGATGCTGTGCGGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 495 AACTCGGAGTGTGCTTACCACACAGACTGTCTTCTTACCAGGCGGCGGCGGCGGCGGCGG 554
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 361 AACTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 555 AAGGCGACCCACAGGCGCTACTGCTGAGGCGGAGGCTGTACCGTGTTCCTTACCTTGTGT 614
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 421 GAAGGTACCATCGCGCTACTGCTTGGAGCGAGGCTGTACCGAGGCTGTACCGAGTCTCCT 480
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 615 GTGTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 644
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 481 GTGTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 510
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
AAA59160
ID AAA59160 standard; cDNA; 985 BP.
XX
AC AAA59160;
XX
DT 07-NOV-2000 (first entry)
XX
DE cDNA encoding a murine interleukin-174 polypeptide.
XX
```

|         |                                                                          |
|---------|--------------------------------------------------------------------------|
| KW      | Interleukin; IL-171; cytokine; CTIA-8; IL-17; IL-175; IL-172; IL-173;    |
| KW      | IL-174; IL-176; IL-177; cell proliferation; cancer; ss.                  |
| XX      |                                                                          |
| Mus sp. |                                                                          |
| OS      |                                                                          |
| FH      | Location/Qualifiers                                                      |
| FT      | 1..510                                                                   |
| CDS     | /*tag= a                                                                 |
| FT      | /product= "interleukin-174"                                              |
| FT      | 1..48                                                                    |
| FT      | /*tag= b                                                                 |
| FT      | mat_peptide                                                              |
| FT      | 49..507                                                                  |
| FT      | /*tag= c                                                                 |
| XX      |                                                                          |
| PX      | WO200042187-A1.                                                          |
| PN      |                                                                          |
| XX      |                                                                          |
| XX      | 20-JUL-2000.                                                             |
| PD      |                                                                          |
| XX      | 10-JAN-2000; 2000WO-US00005.                                             |
| PX      |                                                                          |
| XX      | 11-JAN-1999; 99US-0229402.                                               |
| PR      |                                                                          |
| XX      | (SCHE ) SCHERING CORP.                                                   |
| PA      |                                                                          |
| XX      | Gorman DM, Bazan JF, Kastelein RA;                                       |
| XI      |                                                                          |
| PI      |                                                                          |
| DR      | WPI; 2000-476060/41.                                                     |
| XX      |                                                                          |
| DR      | P-PSDB; AAB07694.                                                        |
| XX      |                                                                          |
| DR      | New DNA sequence encoding a mammalian homolog of CTLA-8, designated      |
| PT      | interleukin-171 (IL-171), useful for recombinant production of IL-171    |
| PT      | which can be used for treating conditions associated with abnormal       |
| PT      | physiology or development -                                              |
| PT      |                                                                          |
| XX      |                                                                          |
| PS      | Disclosure; Page 21; 11pp; English.                                      |
| XX      |                                                                          |
| CC      | The present sequence encodes an interleukin (IL)-174 polypeptide.        |
| CC      | It is a mammalian homologue of the cytokine designated CTIA-8 (also      |
| CC      | referred to as IL-17). The specification also describes homologues       |
| CC      | IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA      |
| CC      | sequence encoding IL-171 is useful for identifying genes, mRNA and       |
| CC      | cDNA molecules which code for related or homologous proteins. The        |
| CC      | IL-171 protein, antibodies against IL-171, and compounds which have      |
| CC      | binding affinity to IL-171 are useful in treatment of conditions         |
| CC      | associated with abnormal physiology or development, including abnormal   |
| CC      | proliferation, e.g. cancerous conditions, or degenerative conditions.    |
| CC      | The IL-171 protein can be used in kits and assay methods for identifying |
| CC      | compounds that selectively bind to IL-171.                               |
| XX      |                                                                          |
| SQ      | Sequence 985 BP; 199 A; 296 C; 268 G; 222 T; 0 other;                    |
|         |                                                                          |
|         | Query Match            52.0%; Score 335.2; DB 21; Length 985;            |
|         | Best Local Similarity   81.0%; Pred. No. 9.1e-81;                        |
|         | Matches   413; Conservative   0; Mismatches   73; Indels   24; Gaps      |
| QY      | 159 ATGTACCAGTGGTTGCATTCTTTGGCAATGGTCATCGGAACCCACACCTACACG----- 212      |
| Db      |                                                                          |
|         | 1 ATGTACCAGGCTGTGTGATTCTTTGGCAATGATCGTGGAAACCCACACCTCAGCTTGCGG 60        |
| QY      | 213 -----CACTGGCCCCAGTGTCTGCCCCAGCAGNAAGGGCAGGACACTCT 254                |
| Db      |                                                                          |
|         | 61 ATCCAGGAGGGCTGCAGTCACTTGTCCCGAGTGTGTGCCCCAGCAAGAGCAAGAACCCTCG 120     |
| QY      | 255 GAGGAGCTGTGAGGTGGAGCATGTGCTGTGCTCCCTCAGCGCTCTAGGCCCTAGGCCCAAC 314    |
| Db      |                                                                          |
|         | 121 GAGGAGTGGCTGAAGTGGAGCTGTGATCTGTGTCTCCCCCAGAGGCTCTGAGCCACAC 180       |
| QY      | 315 CGCACCCAGAGTCCGTGTAGGGCCAGTGAAGATGGAGCCCTCAACAGCAGGGCCATCTCC 374     |
| Db      |                                                                          |
|         | 181 CACCAGCAGAACTCTGCAGGGCCACAGGATGGCCCCCTTAACAGCAGGGCCATCTCT 240        |
| QY      | 375 CCTTGGAGATATGAGTTGGACAGAGACTTGAACCCGGCTCCCCCAGGACCTGTACCACGCC 434    |
|         |                                                                          |

PS Disclosure; Page 28-29; 29pp; English.

XX The invention relates to methods of directing an immune response in a  
CC mammal by the administration of an agonist or antagonist of the cytokine  
CC Interleukin 174 (IL-174). Administration of an IL-174 agonist directs the  
CC immune response towards a Th2 response, stimulates an innate immune  
CC response, augments the inflammatory response from epithelial or  
CC fibroblast cells, induces gut cell growth, promotes extramedullary  
CC hematopoiesis, or augments an antibody response in serum and faecal  
CC material, while administration of an IL-174 antagonist directs the immune  
CC response away from a Th2 type response, and prevents inflammation or  
CC granuloma formation. IL-174 agonists may be used to treat autoimmune  
CC conditions (particularly multiple sclerosis, systemic lupus  
CC erythematosus, rheumatoid arthritis, diabetes or psoriasis), a response  
CC to an infectious agent, or inflammatory conditions such as Crohn's  
CC disease, ulcerative colitis, pancreatitis, or hepatitis. IL-174  
CC antagonists may be used to treat inflammatory, allergic or Th2-mediated  
CC conditions (e.g., systemic anaphylactic response, skin hypersensitivity  
CC response, dermatitis, asthma, fibrosis, or eosinophilic gastritis). The  
CC present sequence represents DNA encoding murine IL-174.

XX  
SQ Sequence 985 BP; 199 A; 296 C; 268 G; 222 T; 0 other;

Query Match 52.08; Score 335.2; DB 24; Length 985;  
Best Local Similarity 81.08; Pred. No. 9.1e-81;  
Matches 413; Conservative 0; Mismatches 73; Indels 24; Gaps 1;

QY 159 ATGTACCAAGCTGGTGGTATCTTGGCATGCTGATGGCAACCCACACCTACAGC----- 212  
Db 1 ATGTACCAAGCTGGTGGTATCTTGGCATGCTGATGGCAACCCACACCTGAGCTGGGG 60

QY 213 -----CACTGGCCAGCTGCTGCCCGCCAGCAAGGCGAGGACACCTCT 254  
Db 61 ATCCAGGAGGCTGCAGTCACTTGCCTGCTGCTGCCCGCCAGCAAGGACACCCCGC 120

QY 255 GAGGAGTGTGAGTGGGAGCACTGTGCTGCTGCTGCCCTAGAGCTGTAGGCCCAAC 314  
Db 121 GAGGAGTGGCTGAAGTGGAGCTGTGCTGCTGCTGCCCGCCAGGAGCTGTAGGCCACAC 180

QY 315 CGCCACCCAGAGTCTCTGAGGCGCCAGTGAAGATGAGCCCTCAACAGCAGGCGCCATCTCC 374  
Db 181 CACCACGAGAACTCTGAGGCGCCAGCAAGATGCGCCCTCAACAGCAGGCGCCATCTCT 240

QY 375 CCCTGGAGATATGATTTGGACAGAGCTTTGAACCGGCTCCCGCCAGGACCTGTACACGCC 434  
Db 241 CCTTGGAGCTATGATTTGGACAGGAGCTTGAATCGGGTCCCGCCAGGACCTGTACACGCT 300

QY 435 CGTTCCCTGTCGCCGCACTGCTGAGCTACAGACAGGCTCCACATGAGCCCGCGGCG 494  
Db 301 CGATGCCCTGTGCCACACTGCGGTGAGCTACAGACAGGCTCCACATGAGCCCGCTGGGC 360

QY 495 AACTCGGAGCTGCTACCAACACAGACTGCTTCTTACCGGCGCCATGCCATGGCGAG 554  
Db 361 AACTCGGCTCCACCTTACCAACACAGAGCTTCTTACCGGCGCCATGCCATGGTGAG 420

QY 555 AAGGCGACCCACAAAGGGCTACTGCTGGAGCGCAGGCTGTACCGGTGTTTCTTAGCTTGT 614  
Db 421 GAAGGTACCCATCGCGCTACTGCTTGGAGCGCAGGCTTACCGAGTCTCTTGGCTTGT 480

QY 615 GTGTGTGTCGGCGCCCGTGTGATGGCTAG 644  
Db 481 GTGTGTGTCGGCGCCCGGTGATGGCTTAG 510

## RESULT 15

AAA58987  
ID AAA58987 standard; cDNA; 620 BP.  
XX  
AC AAA58987;

XX 07-NOV-2000 (first entry)  
DT cDNA encoding a murine interleukin (IL) 174 polypeptide.  
DE

XX Interleukin; IL-17; CTIA-8; IL-170; IL-172; IL-173; IL-174; IL-176;  
KW IL-177; IL-171; cell proliferation; cancer; ss.  
XX Mus sp.  
XX WO200042188-A2.  
XX 20-JUL-2000.  
XX 10-JAN-2000; 2000WO-US000008.  
XX 11-JAN-1999; 99US-0228822.  
XX (SCHE ) SCHERING CORP.  
XX Gorman DM, Bazan JF, Kastelein RA;  
XX WPI; 2000-466130/40.  
XX P-PSDB; AAB07599.  
XX New isolated polynucleotide encoding a mammalian Interleukin-17 like  
PT protein used to identify genes for homologous proteins -  
PT Disclosure; Page 17; 11pp; English.  
XX The present sequence encodes an Interleukin-174 (IL-174) polypeptide.  
CC The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a  
CC member of a new group of interleukins, IL-170 polypeptides. The members  
CC comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170  
CC protein can be used to treat abnormal proliferation e.g. cancer  
CC or degenerative conditions. Antibodies can be used in diagnostic  
CC methods to detect over production of IL-170 protein in cells or body  
CC fluids.

XX  
SQ Sequence 620 BP; 125 A; 183 C; 188 G; 124 T; 0 other;

Query Match 38.8%; Score 249.6; DB 21; Length 620;  
Best Local Similarity 80.1%; Pred. No. 1.1e-57;  
Matches 330; Conservative 0; Mismatches 79; Indels 3; Gaps 3;

QY 233 CAGCAAGGGCAGGACACCTCTGAGGAGCTGCTGAGTGGAGCAGCTGTGCTGTGCTCTCC 292  
Db 1 CGGCACAGGGCGCACAAAGCCCGGAGAGTGGCTGAAGTGGAGCTGTGATCTGTATCCCC 60

QY 293 CCTAGAGCCTGTAGGCCCAACCCGCCAGAGTCTGTAGGGCCAGTGAAGATGGACC 352  
Db 61 CCCAGAGCTCTGAGCCACACCCACGAGAACTCTGAGGGCCAGCAAGATGG-CC 119

QY 353 CCTCAACAGCAGGGCCATCTCCCTGGAGATATGATTTGGACAGAGACTTGAACCGGCT 412  
Db 120 TCTCAACAGCAGGGCCATCTCTCTTGGAGTATGATTTGGACAGGAGCTTGAATCGGGT 179

QY 413 CCCCAGGAGCTGTACCAGCCCGTTCCTGTCGCCGCACTGGCTGAGCTACAGACAGG 472  
Db 180 CCCCAGGAGCTGTACCAGCTGATGCTGTGCCACACTGGCTCAGCTCAGCTACAGACAGG 239

QY 473 CTCACATGAGCCCGGGGCAACTCGGAGCTGTCTTACCAACACAGACTGTCTTCTA 532  
Db 240 CTCACATGAGCCCGCTGGGCAACTCCCTCCACTTTTACCACACAGACAGCTTCTA 299

QY 533 CCGGGCGGCATGCCATGGCGAGAAGGGCACCCCAAGGGCTACTGCTGAGCGCAGGCT 592  
Db 300 CCGGGCGGCATG-CATGGCGAGGAGGTACCCATCCCGCTACTGCTTGGAGCGCAGG-T 357

QY 593 GTACCGTGTTCCTTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 644  
Db 358 CTACCGAGTCTCCTTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 409

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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 12, 2003, 01:11:39 ; Search time 44 Seconds  
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487.576 Million cell updates/sec

Title: US-10-037-591A-2

Perfect score: 910

Sequence: 1 MYQVAFSLAMVMTHTYSHW.....ERRLYRSLACVCRPRVMG 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_101002.\*  
1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
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16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description         |
|------------|-------|-------------|--------|----|---------------------|
| 1          | 910   | 100.0       | 161    | 21 | A human interleukin |
| 2          | 910   | 100.0       | 161    | 21 | A human interleukin |
| 3          | 910   | 100.0       | 161    | 23 | Human interleukin-  |
| 4          | 910   | 100.0       | 161    | 23 | Human interleukin   |
| 5          | 910   | 100.0       | 161    | 23 | Human IL-17 recept  |
| 6          | 898   | 98.7        | 177    | 22 | Human interleukin   |
| 7          | 898   | 98.7        | 177    | 22 | PRO10272 polypepti  |
| 8          | 898   | 98.7        | 177    | 22 | Human PRO10272. H   |
| 9          | 834   | 91.6        | 350    | 22 | Novel human diagno  |
| 10         | 709   | 77.9        | 169    | 21 | A murine interleuk  |

|    |       |      |     |    |          |                    |
|----|-------|------|-----|----|----------|--------------------|
| 11 | 709   | 77.9 | 169 | 21 | AA07694  | A murine interleuk |
| 12 | 709   | 77.9 | 169 | 23 | AAE18121 | Mouse Interleukin- |
| 13 | 709   | 77.9 | 169 | 23 | AA052692 | Murine Interleukin |
| 14 | 670   | 73.6 | 160 | 23 | AAE18122 | Mouse non-secreted |
| 15 | 351.5 | 38.6 | 144 | 21 | AA07599  | A murine interleuk |
| 16 | 351.5 | 38.6 | 144 | 21 | AA07693  | A murine interleuk |
| 17 | 170.5 | 18.7 | 206 | 21 | AA04485  | Human Interleukin  |
| 18 | 165.5 | 18.2 | 187 | 23 | AAE23794 | Mature human LP-48 |
| 19 | 165.5 | 18.2 | 197 | 21 | AAE18911 | A novel polypeptid |
| 20 | 165.5 | 18.2 | 197 | 21 | AA07602  | A human interleuki |
| 21 | 165.5 | 18.2 | 197 | 21 | AA07684  | A human interleuki |
| 22 | 165.5 | 18.2 | 197 | 21 | AA092338 | Human Interleukin- |
| 23 | 165.5 | 18.2 | 197 | 21 | AA04460  | Human Interleukin  |
| 24 | 165.5 | 18.2 | 197 | 21 | AA053892 | Amino acid sequenc |
| 25 | 165.5 | 18.2 | 197 | 22 | AA066121 | Human interleukin  |
| 26 | 165.5 | 18.2 | 197 | 22 | AAU29247 | Human PRO polypept |
| 27 | 165.5 | 18.2 | 197 | 22 | AAU04951 | Human Interleukin  |
| 28 | 165.5 | 18.2 | 197 | 22 | AAE23792 | Human LP-48 protel |
| 29 | 165.5 | 18.2 | 227 | 22 | AAE08676 | Human interleukin  |
| 30 | 165.5 | 18.2 | 227 | 22 | AAE08679 | Human interleukin  |
| 31 | 165.5 | 18.2 | 227 | 22 | AAE08680 | Human interleukin  |
| 32 | 165.5 | 18.2 | 227 | 22 | AAE08681 | Human interleukin  |
| 33 | 165.5 | 18.2 | 227 | 22 | AAE08682 | Human interleukin  |
| 34 | 165.5 | 18.2 | 227 | 22 | AAE08683 | Human interleukin  |
| 35 | 165.5 | 18.2 | 227 | 22 | AAE08684 | Human interleukin  |
| 36 | 165.5 | 18.2 | 425 | 21 | AA04462  | Human Interleukin  |
| 37 | 165   | 18.1 | 223 | 22 | AAE08677 | Human mature inter |
| 38 | 163.5 | 18.0 | 227 | 22 | AAE08685 | Human interleukin  |
| 39 | 161.5 | 17.7 | 227 | 22 | AAE08687 | Human interleukin  |
| 40 | 160.5 | 17.6 | 227 | 22 | AAE08686 | Human interleukin  |
| 41 | 157.5 | 17.3 | 227 | 22 | AAE08690 | Human interleukin  |
| 42 | 156.5 | 17.2 | 227 | 22 | AAE08688 | Human interleukin  |
| 43 | 156.5 | 17.2 | 227 | 22 | AAE08689 | Human interleukin  |
| 44 | 156.5 | 17.2 | 227 | 22 | AAE08691 | Human interleukin  |
| 45 | 156.5 | 17.2 | 227 | 22 | AAE08693 | Human interleukin  |

#### ALIGNMENTS

RESULT 1

AA07598

ID AA07598 standard; Protein; 161 AA.

XX AA07598;

AC AA07598;

XX DT 07-NOV-2000 (first entry)

XX A human interleukin (IL) 174 polypeptide.

XX Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;  
IL-177; IL-171; cell proliferation; cancer.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Peptide 1..16 "signal peptide"

FT Modified-site /note= "calcium phosphorylation site"

FT Modified-site /note= "calcium phosphorylation site"

FT Modified-site /note= "calcium phosphorylation site"

FT Modified-site /note= "myristoylation site"

FT Protein 17..161

FT Modified-site /note= "mature protein"

FT Modified-site /note= "phosphorylation site"

FT Modified-site /note= "phosphorylation site"

FT Modified-site /note= "cAMP protein kinase phosphorylation site"

FT Modified-site /note= "phosphorylation site"

FT Modified-site /note= "phosphorylation site"

FT Modified-site /note= "phosphorylation site"

FT Modified-site /note= "phosphorylation site"

FT Modified-site /note= "phosphorylation site"

FT Modified-site /note= "phosphorylation site"

FT Modified-site /note= "phosphorylation site"

FT Modified-site /note= "phosphorylation site"

FT Modified-site /note= "protein kinase C phosphorylation site"  
FT 43  
FT Modified-site /note= "phosphorylation site"  
FT 45..47  
FT Modified-site /note= "calcium phosphorylation site"  
FT 53  
FT Modified-site /note= "phosphorylation site"  
FT 53..56  
FT Modified-site /note= "cAMP protein kinase phosphorylation site"  
FT 56  
FT Modified-site /note= "phosphorylation site"  
FT 95  
FT Modified-site /note= "phosphorylation site"  
FT 95..98  
FT Modified-site /note= "cAMP protein kinase phosphorylation site"  
FT 95..102  
FT Modified-site /note= "tyrosine kinase site"  
FT 98  
FT Modified-site /note= "phosphorylation site"  
FT 104..107  
FT Modified-site /note= "N-glycosylation site"  
FT 115..119  
FT Modified-site /note= "myristoylation site"  
FT 118..122  
FT Modified-site /note= "myristoylation site"  
FT 119..121  
FT Modified-site /note= "protein kinase C phosphorylation site"  
FT 131  
FT Modified-site /note= "phosphorylation site"  
XX  
PN WO200042188-A2.  
XX  
XX 20-JUL-2000.  
XX  
XX 10-JAN-2000; 2000WO-US00006.  
XX  
XX 11-JAN-1999; 99US-0228822.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
XX Gorman DM, Bazan JF, Kastelein RA;  
XX  
XX WPI; 2000-466130/40.  
DR N-PSDB; AAA58986.  
XX  
XX New isolated polynucleotide encoding a mammalian Interleukin-17 like  
PT protein used to identify genes for homologous proteins  
XX  
XX Claim 11; Page 16; 11lpp; English.  
XX  
XX The present sequence represents an interleukin-174 (IL-174) polypeptide.  
CC The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a  
CC member of a new group of interleukins, IL-170 polypeptides. The members  
CC comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170  
CC protein can be used to treat abnormal proliferation e.g. cancer  
CC or degenerative conditions. Antibodies can be used in diagnostic  
CC methods to detect over production of IL-170 protein in cells or body  
CC fluids.  
XX  
XX Sequence 161 AA;  
SQ  
Query Match 100.0%; Score 910; DB 21; Length 161;  
Best Local Similarity 100.0%; Pred. No. 4.1e-86;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MYQVAFAMVMGTHYSHWPCSCPSKQDTSEELLRWSTVPVPLEPARNRHPSERA 60  
DB 1 MYQVAFAMVMGTHYSHWPCSCPSKQDTSEELLRWSTVPVPLEPARNRHPSERA 60  
QY 61 SEDGPLNSRAISPMRYELDRDLNRLPDQLYHARCLPHCVSLQTGSHWDPGNSSELLYHN 120  
DB 61 SEDGPLNSRAISPMRYELDRDLNRLPDQLYHARCLPHCVSLQTGSHWDPGNSSELLYHN 120

QY 121 QTVFYRRPCHGEKCTHKGYCLERLYRVSLACVCRPRVMG 161  
DB 121 QTVFYRRPCHGEKCTHKGYCLERLYRVSLACVCRPRVMG 161  
RESULT 2  
AAB07692  
ID AAB07692 standard; Protein: 161 AA.  
XX  
XX AAB07692;  
XX  
XX 07-NOV-2000 (first entry)  
XX  
XX A human interleukin-174 polypeptide.  
XX  
XX Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;  
KW IL-174; IL-176; IL-177; cell proliferation; cancer.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..16  
FT /note= "signal peptide"  
FT  
FT Modified-site 15..17 "calcium phosphorylation site"  
FT /note= "calcium phosphorylation site"  
FT 16..18  
FT Modified-site 12..16  
FT /note= "myristoylation site"  
FT Protein 17..161  
FT /note= "mature protein"  
FT Modified-site 21  
FT /note= "phosphorylation site"  
FT Modified-site 21..24  
FT /note= "cAMP protein kinase phosphorylation site"  
FT Modified-site 23  
FT /note= "phosphorylation site"  
FT Modified-site 41..43  
FT /note= "protein kinase C phosphorylation site"  
FT Modified-site 43  
FT /note= "phosphorylation site"  
FT Modified-site 45..47  
FT /note= "calcium phosphorylation site"  
FT Modified-site 53  
FT /note= "phosphorylation site"  
FT Modified-site 53..56  
FT /note= "cAMP protein kinase phosphorylation site"  
FT Modified-site 56  
FT /note= "phosphorylation site"  
FT Modified-site 95  
FT /note= "phosphorylation site"  
FT Modified-site 95..98  
FT /note= "cAMP protein kinase phosphorylation site"  
FT Modified-site 95..102  
FT /note= "tyrosine kinase site"  
FT Modified-site 98  
FT /note= "phosphorylation site"  
FT Modified-site 104..107  
FT /note= "N-glycosylation site"  
FT Modified-site 115..119  
FT /note= "myristoylation site"  
FT Modified-site 118..122  
FT /note= "myristoylation site"  
FT Modified-site 119..121  
FT /note= "protein kinase C phosphorylation site"  
FT Modified-site 131  
FT /note= "phosphorylation site"  
XX  
XX WO200042187-A1.  
XX  
XX 20-JUL-2000.  
XX  
XX 10-JAN-2000; 2000WO-US00005.



11-JAN-1999; 99US-0229402.  
 (SCHE ) SCHERING CORP.  
 Gorman DM, Bazan JF, Kastelein RA;  
 WPI; 2000-476060/41.  
 N-PSDB; AAA59158.  
 New DNA sequence encoding a mammalian homolog of CTLA-8, designated  
 interleukin-171 (IL-171), useful for recombinant production of IL-171  
 which can be used for treating conditions associated with abnormal  
 physiology or development  
 Disclosure; Page 19; 11pp; English.  
 The present sequence represents an interleukin (IL)-174 polypeptide.  
 It is a mammalian homologue of the cytokine designated CTLA-8 (also  
 referred to as IL-17). The specification also describes homologues  
 IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA  
 sequence encoding IL-171 is useful for identifying genes, mRNA and  
 cDNA molecules which code for related or homologous proteins. The  
 IL-171 protein, antibodies against IL-171, and compounds which have  
 binding affinity to IL-171 are useful in treatment of conditions  
 associated with abnormal physiology or development, including abnormal  
 proliferation, e.g. cancerous conditions, or degenerative conditions.  
 The IL-171 protein can be used in kits and assay methods for identifying  
 compounds that selectively bind to IL-171.  
 Sequence 161 AA;  
 Query Match 100.0%; Score 910; DB 21; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-86;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MYQVVAFLAMVWGTHYSHWPCSCPSKGGDTSEELLRWSTVPVPLEPARNRHPESCRA 60  
 DB 1 MYQVVAFLAMVWGTHYSHWPCSCPSKGGDTSEELLRWSTVPVPLEPARNRHPESCRA 60  
 QY 61 SEDGPLNSRAISPWRYELDRDLNRLPDQLYHARCLPCHVCVSLQTGSHMDPRGNSSELYHN 120  
 DB 61 SEDGPLNSRAISPWRYELDRDLNRLPDQLYHARCLPCHVCVSLQTGSHMDPRGNSSELYHN 120  
 QY 121 QTVFYRRPCHGKGTGKCYCLERRLYRVSLACVCRVRVMG 161  
 DB 121 QTVFYRRPCHGKGTGKCYCLERRLYRVSLACVCRVRVMG 161  
 RESULT 3  
 ID AAE18120 standard; Protein; 161 AA.  
 XX AAE18120;  
 XX AC  
 XX XX  
 DT 07-MAY-2002 (first entry)  
 XX  
 DE Human Interleukin-17 like (IL-17L) protein.  
 XX  
 KW Human; interleukin-17 like; IL-17L; immune system dysfunction; diabetes;  
 KW cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;  
 KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;  
 KW autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;  
 KW infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;  
 KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;  
 KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;  
 KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;  
 KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;  
 KW cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers

FT Peptide 1..16 /label= Signal\_peptide  
 FT Protein 17..161 /label= Mature\_IL\_17L\_protein  
 XX WO200208285-A2.  
 PD 31-JAN-2002.  
 XX 21-JUN-2001; 2001WO-US19861.  
 XX 22-JUN-2000; 2000US-213125P.  
 PR 02-FEB-2000; 2001US-266159P.  
 PR 16-MAR-2001; 2001US-0810384.  
 XX (AMGE-) AMGEN INC.  
 PA Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S;  
 PI WPI; 2002-155217/20.  
 DR N-PSDB; AAD28771.  
 XX Nucleic acid molecules encoding Interleukin 17 (IL-17) - like  
 PT polypeptides useful in the treatment, prevention and diagnosis of  
 XX diseases e.g. cancer  
 PS Claim 13; Fig 1; 242pp; English.  
 XX The invention relates to nucleic acid molecules encoding Interleukin 17  
 CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels  
 CC of IL-17 protein in an animal. The IL-17 protein is useful for treating,  
 CC preventing or ameliorating a disease, such as immune system dysfunction  
 CC (rheumatoid arthritis, osteoarthritis, inflammatory joint disease);  
 CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel  
 CC disease, transplant rejection, graft vs. host disease); infections (HIV,  
 CC hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,  
 CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung  
 CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin  
 CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone  
 CC (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy  
 CC atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma  
 CC leukaemia); reproductive (infertility, miscarriage, endometriosis), eye  
 CC (blindness, retinal neuropathy) and treatment of diseases involving  
 CC inflammation. The present sequence is human Interleukin-17 like (IL-17L)  
 CC protein.  
 XX Sequence 161 AA;  
 QY Query Match 100.0%; Score 910; DB 23; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-86;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MYQVVAFLAMVWGTHYSHWPCSCPSKGGDTSEELLRWSTVPVPLEPARNRHPESCRA 60  
 DB 1 MYQVVAFLAMVWGTHYSHWPCSCPSKGGDTSEELLRWSTVPVPLEPARNRHPESCRA 60  
 QY 61 SEDGPLNSRAISPWRYELDRDLNRLPDQLYHARCLPCHVCVSLQTGSHMDPRGNSSELYHN 120  
 DB 61 SEDGPLNSRAISPWRYELDRDLNRLPDQLYHARCLPCHVCVSLQTGSHMDPRGNSSELYHN 120  
 QY 121 QTVFYRRPCHGKGTGKCYCLERRLYRVSLACVCRVRVMG 161  
 DB 121 QTVFYRRPCHGKGTGKCYCLERRLYRVSLACVCRVRVMG 161  
 RESULT 4  
 ID AAM52691 standard; Protein; 161 AA.  
 XX AAM52691;  
 XX AC  
 XX XX  
 DT 26-FEB-2002 (first entry)  
 XX

DE Human interleukin 174 (IL-174).  
 XX  
 KW Human; interleukin 174; IL-174; cytokine; Th2 response;  
 KW innate immune response; inflammation; gut cell growth;  
 KW extramedullary haematopoiesis; antibody response; granuloma formation;  
 KW autoimmune condition; multiple sclerosis; systemic lupus erythematosus;  
 KW rheumatoid arthritis; diabetes; psoriasis; infectious agent;  
 KW inflammatory condition; Crohn's disease; ulcerative colitis;  
 KW pancreatitis; hepatitis; allergy; Th2-mediated condition;  
 KW systemic anaphylactic response; skin hypersensitivity response;  
 KW dermatitis; asthma; fibrosis; eosinophilic gastritis; immunomodulator;  
 KW antiinflammatory; antiarthritic; antidiabetic; antifungal;  
 KW dermatological; neuroprotective; antiallergic; agonist; antagonist.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX Peptide 1..16  
 XX /label= Signal\_peptide  
 XX Protein 17..161  
 XX /label= Mature\_IL-174  
 XX WO200179288-A2.  
 XX 25-OCT-2001.  
 XX 17-APR-2001; 2001WO-US12493.  
 XX 18-APR-2000; 2000US-198488P.  
 XX (SCHE ) SCHERING CORP.  
 XX Hurst SD, Zurawski SM, Rennick DM;  
 XX WPI; 2002-034343/04.  
 XX N-PSDB; ABA02393.  
 XX Administering an interleukin 174 agonist or antagonist to a mammal  
 XX regulates various immune and inflammatory responses and is useful to  
 XX treat for example autoimmune diseases, allergies or response to an  
 XX infection -  
 XX Examples; Page 27-28; 29pp; English.  
 XX  
 CC The invention relates to methods of directing an immune response in a  
 CC mammal by the administration of an agonist or antagonist of the cytokine  
 CC interleukin 174 (IL-174). Administration of an IL-174 agonist directs the  
 CC immune response towards a Th2 response, stimulates an innate immune  
 CC response, augments the inflammatory response from epithelial or  
 CC fibroblast cells, induces gut cell growth, promotes extramedullary  
 CC haematopoiesis, or augments an antibody response in serum and faecal  
 CC material, while administration of an IL-174 antagonist directs the immune  
 CC response away from a Th2 type response, and prevents inflammation or  
 CC granuloma formation. IL-174 agonists may be used to treat autoimmune  
 CC conditions (particularly multiple sclerosis, systemic lupus  
 CC erythematosus, rheumatoid arthritis, diabetes or psoriasis), a response  
 CC to an infectious agent, or inflammatory conditions such as Crohn's  
 CC disease, ulcerative colitis, pancreatitis, or hepatitis. IL-174  
 CC antagonists may be used to treat inflammatory, allergic or Th2-mediated  
 CC conditions (e.g., systemic anaphylactic response, skin hypersensitivity  
 CC response, dermatitis, asthma, fibrosis, or eosinophilic gastritis). The  
 CC present sequence represents human IL-174.  
 XX  
 XX Sequence 161 AA;  
 XX  
 Query Match 100.0%; Score 910; DB 23; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-86;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYQVAFVFLVNGTHTYSHWPSCCPSKQDTSEELLRWSTVPVPLEPARNRHPESCRA 60  
 DB 1 MYQVAFVFLVNGTHTYSHWPSCCPSKQDTSEELLRWSTVPVPLEPARNRHPESCRA 60

Qy 61 SEDGPLNSRAISPMRYELDRDLNRLPQDLYHARCLCPHCVSLOTGSHMDPRGNSELLYHN 120  
 Db 61 SEDGPLNSRAISPMRYELDRDLNRLPQDLYHARCLCPHCVSLOTGSHMDPRGNSELLYHN 120  
 Qy 121 QTVFYRRPCHGKGTGKGYCLERRLYRVSACVCVRPRVMG 161  
 Db 121 QTVFYRRPCHGKGTGKGYCLERRLYRVSACVCVRPRVMG 161  
 RESULT 5  
 AAM47464  
 ID AAM47464 standard; Protein; 161 AA.  
 XX AAM47464;  
 XX 11-FEB-2002 (first entry)  
 XX Human IL-17 receptor like protein ligand, IL-17E.  
 DE Human; IL-17 receptor-like protein; immunomodulatory; antiarthritic;  
 KW antipsoriatic; antimicrobial; anorectic; nootropic; neuroprotective;  
 KW antischmatic; antiallergic; dermatological; cytostatic; gene therapy;  
 KW interleukin 17; immune system disorder; infection; weight; reproductive;  
 KW neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation;  
 KW glomerulonephritis; bone; osteoporosis; vascular system; ischaemia; eye;  
 KW tumour; IL-17E.  
 XX  
 OS Homo sapiens.  
 XX WO200168705-A2.  
 XX 20-SEP-2001.  
 XX 16-MAR-2001; 2001WO-US08688.  
 XX 16-MAR-2000; 2000US-189923P.  
 XX 12-MAY-2000; 2000US-204208P.  
 XX 27-NOV-2000; 2000US-072322.  
 XX 02-FEB-2001; 2001US-266159P.  
 XX (AMGE-) AMGEN INC.  
 XX Jing S, Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ;  
 WPI; 2002-055100/07.  
 N-PSDB; ABA03213.  
 Three human nucleic acids encoding interleukin 17 (IL-17) receptor like  
 polypeptides, useful for treating, diagnosing, ameliorating or  
 preventing immune system disorders (e.g. psoriatic arthritis) and  
 infections (e.g. viral infections) -  
 Example 7; Page 234-235; 239pp; English.  
 The present invention relates to novel human nucleic acids encoding  
 interleukin 17 (IL-17) receptor like proteins (see ABA03200-ABA03202,  
 AAM47456, AAM47458 and AAM47459). The IL-17 receptor-like proteins and  
 coding sequences are useful for treating a pathological condition related  
 to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g.  
 viral infections), weight disorders (e.g. obesity), neuronal dysfunction  
 disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin  
 disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis),  
 bone disease (e.g. osteoporosis), vascular system disorders (e.g.  
 ischaemia), eye disorders, reproductive disorders, tumours and  
 inflammation. The present sequence is the protein sequence for IL-17E, a  
 human IL-17 receptor like protein ligand.  
 XX  
 XX Sequence 161 AA;  
 XX  
 Query Match 100.0%; Score 910; DB 23; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-86;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYQVAFAMVGTHTYSHWPCSCPSKQDTSSELLRWSTVPVPPLEPARPNRHPESCA 60  
 Db 1 MYQVAFAMVGTHTYSHWPCSCPSKQDTSSELLRWSTVPVPPLEPARPNRHPESCA 60  
 QY 61 SEDGPLNSRAISPRWYELDRDLNRLPQDLYHARCLCPHCVSLQTSQSHMDPRGNSSELLYHN 120  
 Db 61 SEDGPLNSRAISPRWYELDRDLNRLPQDLYHARCLCPHCVSLQTSQSHMDPRGNSSELLYHN 120  
 QY 121 QTVFYRRPCHGKGTGKGYCLERRLYRVSLACVVCVRPVYMG 161  
 Db 121 QTVFYRRPCHGKGTGKGYCLERRLYRVSLACVVCVRPVYMG 161  
 RESULT 6  
 AAU04952  
 ID AAU04952 standard; Protein; 177 AA.  
 AC AAU04952;  
 XX  
 XX  
 XX 24-OCT-2001 (first entry)  
 XX Human Interleukin 17E ligand, IL-17E.  
 XX  
 KW Human; Interleukin-17E ligand; IL-17E; agonist; antagonist;  
 KW PRO10272; DNA 147531-2821; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;  
 KW allergic disease; asthma; demyelinating disease;  
 KW degenerative cartilaginous disorder; transplantation associated disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Peptide  
 FT 1..32 Location/Qualifiers  
 FT /label= Signal\_peptide  
 FT 33..177  
 FT /label= Mature\_IL\_17E  
 FT 44..50  
 FT /note= "N-myristoylation site"  
 FT 127..135  
 FT /note= "Tyrosine kinase phosphorylation site"  
 FT 136..140  
 FT /note= "Asn is glycosylated"  
 FT 150..156  
 FT /note= "N-myristoylation site"  
 XX  
 XX WO200146420-A2.  
 XX  
 XX 28-JUN-2001.  
 XX  
 XX 20-DEC-2000; 2000WO-US34956.  
 XX  
 XX 23-DEC-1999; 99US-0172096.  
 XX 30-DEC-1999; 99WO-US31274.  
 XX 11-JAN-2000; 2000US-0175481.  
 XX 18-FEB-2000; 2000WO-US04341.  
 XX 02-MAR-2000; 2000WO-US05841.  
 XX 21-MAR-2000; 2000US-0191007.  
 XX 21-MAR-2000; 2000WO-US07532.  
 XX 02-JUN-2000; 2000WO-US5264.  
 XX 22-JUN-2000; 2000US-0213087.  
 XX 22-AUG-2000; 2000US-0644848.  
 XX 24-AUG-2000; 2000WO-US23328.  
 XX 24-OCT-2000; 2000US-0242837.  
 XX 10-NOV-2000; 2000WO-US30873.  
 XX 28-NOV-2000; 2000US-0253646.  
 XX 01-DEC-2000; 2000WO-US32678.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;  
 PI Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RL;  
 PI Watanabe CK, Williams PM, Wood WI, Yansura DG;  
 XX

DR WPI; 2001-451708/48.  
 XX N-PSDB; AAS09511.  
 XX  
 PT Novel PRO polypeptides homologous to interleukin-17, useful for the  
 PT diagnosis and treatment of immune related disease e.g. rheumatoid  
 PT arthritis and diabetes  
 XX  
 PS Claim 10; Fig 6; 188pp; English.  
 XX  
 XX The sequence is PRO10272 which is the human Interleukin 17E ligand,  
 CC IL-17E, encoded by DNA 147531-2821. A composition  
 CC containing ant/agonists to the PRO polypeptides or individual components  
 CC are useful for treating a mammal with an immune related disease, e.g.  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 CC disease, contact dermatitis, an autoimmune or immune-mediated skin  
 CC disease, contact dermatitis, an allergic disease e.g. food  
 CC hypersensitivity, asthma, a transplantation associated disease, or a  
 CC chronic inflammatory demyelinating polyneuropathy. Treating a  
 CC degenerative cartilaginous disorder comprises administering a PRO1031 or  
 CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous  
 CC examples of the diseases and disorders are given in the specification.  
 XX  
 XX Sequence 177 AA;  
 SQ  
 Query Match 98.7%; Score 898; DB 22; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-85;  
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QVVAFLAMVGTHTYSHWPCSCPSKQDTSSELLRWSTVPVPPLEPARPNRHPESCA 62  
 Db 19 QVVAFLAMVGTHTYSHWPCSCPSKQDTSSELLRWSTVPVPPLEPARPNRHPESCA 78  
 QY 63 DGPLNSRAISPRWYELDRDLNRLPQDLYHARCLCPHCVSLQTSQSHMDPRGNSSELLYHNQT 122  
 Db 79 DGPLNSRAISPRWYELDRDLNRLPQDLYHARCLCPHCVSLQTSQSHMDPRGNSSELLYHNQT 138  
 QY 123 VFYRRPCHGKGTGKGYCLERRLYRVSLACVVCVRPVYMG 161  
 Db 139 VFYRRPCHGKGTGKGYCLERRLYRVSLACVVCVRPVYMG 177  
 RESULT 7  
 AAB47299  
 ID AAB47299 standard; Protein; 177 AA.  
 XX  
 XX AAB47299;  
 XX  
 XX 22-AUG-2001 (first entry)  
 XX  
 XX PRO10272 polypeptide.  
 XX  
 XX PRO; PRO1081; PRO1274; PRO10272; proliferation; T-lymphocyte;  
 KW PRO1199; PRO1556; PRO4401; PRO10268; inhibition; stimulation;  
 KW infiltration; mononuclear cell; eosinophil; erythema multiforme;  
 KW polymorphonuclear neutrophil; PMN; antibody; immune-related disorder;  
 KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;  
 KW juvenile chronic arthritis; spondyloarthropathy; systemic sclerosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; skin disease;  
 KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anemia; asthma;  
 KW autoimmune thrombocytopaenia; thyroiditis; diabetes mellitus; allergy;  
 KW immune-mediated renal disease; demyelination; central nervous system;  
 KW peripheral nervous system; idiopathic demyelinating polyneuropathy;  
 KW Guillain-Barre syndrome; hepatobiliary disease; eosinophilic pneumonia;  
 KW chronic active hepatitis; primary biliary cirrhosis; allergic rhinitis;  
 KW granulomatous hepatitis; sclerosing cholangitis; food hypersensitivity;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy; urticaria;  
 KW Whipple's disease; idiopathic pulmonary fibrosis; contact dermatitis;  
 KW psoriasis; atopic dermatitis; hypersensitivity pneumonitis;  
 KW graft rejection; graft-versus-host disease.

XX OS Homo sapiens.  
XX FH Key  
XX FT Peptide  
XX FT /label- Signal peptide  
XX FT Protein  
XX FT /label- Mature PRO10272  
XX FT Modified-site  
XX FT /label- N-myristoylation site  
XX FT Modified-site  
XX FT /label- Tyrosine kinase phosphorylation site  
XX FT Modified-site  
XX FT /label- N-glycosylation site  
XX FT Modified-site  
XX FT /label- N-myristoylation site  
XX PN WO200140465-A2.  
XX PD 07-JUN-2001.  
XX PF 10-NOV-2000; 2000WO-US30873.  
XX PR 30-NOV-1999; 99WO-US28313.  
XX PR 09-DEC-1999; 99US-0170262.  
XX PR 23-DEC-1999; 99US-0172059.  
XX PR 11-JAN-2000; 2000US-0175481.  
XX PR 20-JAN-2000; 2000US-0177118.  
XX PR 18-FEB-2000; 2000WO-US04342.  
XX PR 03-MAR-2000; 2000US-0187202.  
XX PR 30-MAY-2000; 2000WO-US14941.  
XX PR 05-JUN-2000; 2000US-0209832.  
XX PR 24-AUG-2000; 2000WO-US23328.  
XX PA (GETH ) GENENTECH INC.  
XX PI Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
XX PI Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX PI WPI; 2001-381384/40.  
XX DR N-PSDB; AAC85969.  
XX XX Isolated PRO polypeptide useful for treat or diagnose an immune-related  
XX PT disorder e.g. arthritis, asthma, allergy, diabetes or psoriasis -  
XX PS Claim 1; Fig 18; 124pp; English.  
XX XX The sequences given in AAB47291-99 show PRO polypeptides. PRO1081,  
XX CC PRO1274 and PRO10272 stimulate the proliferation of T-lymphocytes and  
XX CC PRO1199, PRO1556, PRO4401 and PRO10268 inhibit the proliferation of  
XX CC T-lymphocytes. PRO1754 and PRO9912 act to enhance the infiltration of  
XX CC mononuclear cells, eosinophils or polymorphonuclear neutrophils (PMN)  
XX CC into the tissue of a mammal. The PRO cDNA's and antibodies which  
XX CC bind to them, are used to treat an immune-related disorder in a  
XX CC mammal. Such disorders include systemic lupus erythematosus,  
XX CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a  
XX CC spondyloarthopathy, systemic sclerosis, an idiopathic inflammatory  
XX CC myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,  
XX CC autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis,  
XX CC diabetes mellitus, immune-mediated renal disease, a demyelinating  
XX CC disease of the central or peripheral nervous system, idiopathic  
XX CC demyelinating polynuropathy, Guillain-Barre syndrome, a chronic  
XX CC inflammatory demyelinating polynuropathy, a hepatobiliary disease,  
XX CC infectious or autoimmune chronic active hepatitis, primary biliary  
XX CC cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
XX CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
XX CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
XX CC disease, erythema multiforme, contact dermatitis, psoriasis, an  
XX CC allergic disease, asthma, allergic rhinitis, atopic dermatitis, food  
XX CC hypersensitivity, urticaria, an immunologic disease of the lung,  
XX CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
XX CC pneumonitis, a transplantation associated disease, graft rejection or  
XX CC graft-versus-host disease.

XX SQ Sequence 177 AA;  
XX Query Match  
XX Best Local Similarity 98.7%; Score 898; DB 22; Length 177;  
XX Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX QY 3 QVVAFLAMVGMTHYSHWPSCCPKQDTSSELLRWSTVPVPPLEPARPNRHPSCRASE 62  
XX DB 19 QVVAFLAMVGMTHYSHWPSCCPKQDTSSELLRWSTVPVPPLEPARPNRHPSCRASE 78  
XX QY 63 DGPLNSRAISPMRYELDRDLNRLPQDLYHARCLCPHCVSLOTGSHMDPRGNSSELLYHNQT 122  
XX DB 79 DGPLNSRAISPMRYELDRDLNRLPQDLYHARCLCPHCVSLOTGSHMDPRGNSSELLYHNQT 138  
XX QY 123 VFYRRPCHGCKGTHKGYCLERRLYRVSLACVVCVRPRVMG 161  
XX DB 139 VFYRRPCHGCKGTHKGYCLERRLYRVSLACVVCVRPRVMG 177  
XX RESULT 8  
XX AAB87603  
XX ID AAB87603 standard; Protein; 177 AA.  
XX AC AAB87603;  
XX XX  
XX DT 15-MAY-2001 (first entry)  
XX DE Human PRO10272.  
XX XX  
XX KW Human; PRO protein; mapping.  
XX OS Homo sapiens.  
XX PN WO200116318-A2.  
XX PD 08-MAR-2001.  
XX PF 24-AUG-2000; 2000WO-US23328.  
XX PR 01-SEP-1999; 99WO-US20111.  
XX PR 15-SEP-1999; 99WO-US21090.  
XX PR 07-DEC-1999; 99US-0169495.  
XX PR 09-DEC-1999; 99US-0170262.  
XX PR 11-JAN-2000; 2000US-0175481.  
XX PR 18-FEB-2000; 2000WO-US04341.  
XX PR 18-FEB-2000; 2000WO-US04342.  
XX PR 22-FEB-2000; 2000WO-US04414.  
XX PR 01-MAR-2000; 2000WO-US05601.  
XX PR 03-MAR-2000; 2000US-0187202.  
XX PR 25-APR-2000; 2000US-0199397.  
XX PR 22-MAY-2000; 2000WO-US14042.  
XX PR 05-JUN-2000; 2000US-0209832.  
XX XX (GETH ) GENENTECH INC.  
XX PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
XX PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;  
XX PI WPI; 2001-183260/18.  
XX DR N-PSDB; AAF92135.  
XX XX Eighty four nucleic acids encoding PRO polypeptides, useful in  
XX PT molecular biology, including use as hybridization probes, and in  
XX PT chromosome and gene mapping.  
XX PT Claim 12; Fig 156; 278pp; English.  
XX PS The present sequence is a human PRO polypeptide (secreted and  
XX CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or  
XX CC anti-PRO antibodies are useful for preparation of a medicament useful in  
XX CC the treatment of a condition which is responsive to the PRO protein,  
XX CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be

CC employed as molecular weight markers for protein electrophoresis. The PRO  
CC coding sequence has applications in molecular biology, including use as  
CC hybridisation probes, and in chromosome and gene mapping.  
XX  
SQ Sequence 177 AA;

Query Match 98.7%; Score 898; DB 22; Length 177;  
Best Local Similarity 100.0%; Pred. No. 8.1e-85;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QVVAFLAMVMTHTYSHWPCSCPSKQDTSSELLRWSTVPVPPLEPARNRHPESCRASE 62  
Db 19 QVVAFLAMVMTHTYSHWPCSCPSKQDTSSELLRWSTVPVPPLEPARNRHPESCRASE 78  
QY 63 DGPLNSRAISPRYELDRDLNLPQDLYHARCLCHVCVSLQTGSHMDPRGNSSELYHNQ 122  
Db 79 DGPLNSRAISPRYELDRDLNLPQDLYHARCLCHVCVSLQTGSHMDPRGNSSELYHNQ 138  
QY 123 VFYRPPCHGEKTHGYCLERRLRYVSLACVCRPRVMG 161  
Db 139 VFYRPPCHGEKTHGYCLERRLRYVSLACVCRPRVMG 177

RESULT 9  
ABG29372  
ID ABG29372 standard; Protein; 350 AA.  
XX  
AC ABG29372;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #29363.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
PR 23-APR-2000; 2000US-0649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
DR N-PSDB; AAS93559.  
XX

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity  
XX

PS Claim 20; SEQ ID No 59731; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 350 AA;

Query Match 91.6%; Score 834; DB 22; Length 350;  
Best Local Similarity 91.1%; Pred. No. 7.8e-78;  
Matches 153; Conservative 1; Mismatches 4; Indels 10; Gaps 2;

QY 3 QVVAFLAMVMTHTYSHWPCSCPSKQDTSSELLRWSTVPVPPLEPARNRHPESCRASE 62  
Db 28 RVVAFLAMVMTHTYSHWPCSCPSKQDTSSELLRWSTVPVPPLEPARNRHPESCRASE 87  
QY 63 DGPLNSRAISPRYELDRDLNLPQDLYHARCLCHVCVSLQTGSHMDPRGNS 114  
Db 88 DGPLNSRAISPRYELDRDLNLPQDLYHARCLCHVCVSLQTGSHMDPRGNS 147  
QY 115 ELLYHNQTVFYRPPCHGEKTHGYCLERRLRYVSLACVCRPRVM 160  
Db 148 ELLYHNQTVFYRPPCHGEKTHGYCLERRLRYVSLACVCRPRVM 195

RESULT 10  
AAB07600  
ID AAB07600 standard; Protein; 169 AA.  
XX  
AC AAB07600;  
XX  
DT 07-NOV-2000 (first entry)  
XX  
DE A murine interleukin (IL) 174 polypeptide.  
XX  
KW Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;  
KW IL-177; IL-171; cell proliferation; cancer.  
XX  
OS Mus sp.

XX  
FH Key Location/Qualifiers  
FT Peptide 1..16 /note= "signal peptide"  
FT Modified-site 2..4 /note= "protein kinase C phosphorylation site"  
FT Protein 17..169 /note= "mature protein"  
FT Modified-site 18..20 /note= "calcium phosphorylation site"  
FT Modified-site 29..32 /note= "CAMP protein kinase phosphorylation site"  
FT Modified-site 29 /note= "phosphorylation site"  
FT Modified-site 31 /note= "phosphorylation site"  
FT Modified-site 49..51 /note= "protein kinase C phosphorylation site"  
FT Modified-site 51 /note= "phosphorylation site"  
FT Modified-site 53 /note= "phosphorylation site"  
FT Modified-site 53..55 /note= "calcium phosphorylation site"  
FT Modified-site 61 /note= "phosphorylation site"  
FT Modified-site 61..64 /note= "CAMP protein kinase phosphorylation site"  
FT Modified-site 64 /note= "phosphorylation site"

FT Modified-site 67...69 /note= "calcium phosphorylation site"  
FT Modified-site 112...114 /note= "N-glycosylation site"  
FT Modified-site 123...127 /note= "myristoylation site"  
FT Modified-site 127...129 /note= "protein kinase C phosphorylation site"  
FT Modified-site 139 /note= "phosphorylation site"  
FT Modified-site 141 /note= "phosphorylation site"

XX WO200042188-A2.

XX 20-JUL-2000.

XX 10-JAN-2000; 2000WO-US000006.

XX 11-JAN-1999; 99US-0228822.

XX (SCHE ) SCHERING CORP.

XX Gorman DM, Bazan JF, Kastelein RA;

XX WPI; 2000-466130/40.

XX N-PSDB; AAA58988.

XX New isolated polynucleotide encoding a mammalian Interleukin-17 like  
PT protein used to identify genes for homologous proteins -

XX Claim 11; Page 18; 11lpp; English.

XX The present sequence represents an interleukin-174 (IL-174) polypeptide.  
CC The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a  
CC member of a new group of interleukins, IL-170 polypeptides. The members  
CC comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170  
CC protein can be used to treat abnormal proliferation e.g. cancer  
CC or degenerative conditions. Antibodies can be used in diagnostic  
CC methods to detect over production of IL-170 protein in cells or body  
CC fluids.

XX Sequence 169 AA;

Query Match 77.9%; Score 709; DB 21; Length 169;

Best Local Similarity 76.8%; Pred. No. 2.7e-65;

Matches 129; Conservative 9; Mismatches 22; Indels 8; Gaps 1;

QY 1 MYQVAFAMVYMGTHY-----SHWPCPCPKGQDTSELLRWSTVPVPPLEPARPN 52

Db 1 MYQVAFAMVYMGTHY-----SHWPCPCPKGQDTSELLRWSTVPVPPLEPARPN 52

QY 53 RHPSCRASEDGPNLSRAISPRVYELDRNLNLPDLYHARCLCPHCYSLOTGSHMDPRG 112

Db 61 HHAESCRASKDGNLSRAISPRVYELDRNLNLPDLYHARCLCPHCYSLOTGSHMDPLG 120

QY 113 NSELLYHNOTVYFRRPCHGEGTHKGYCLERRLYRVSILACVCVRPRVM 160

Db 121 NSVPLYHNOTVYFRRPCHGEGTHKGYCLERRLYRVSILACVCVRPRVM 168

RESULT 11

AAB07694

ID AAB07694 standard; Protein; 169 AA.

XX AAB07694;

XX 07-NOV-2000 (first entry)

XX A murine interleukin-174 polypeptide.

XX Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;  
KW IL-174; IL-176; IL-177; cell proliferation; cancer.

XX Mus sp.  
OS Key  
PH Peptide  
FT Location/Qualifiers  
FT 1..16 "signal peptide"  
FT 2..4 /note= "protein kinase C phosphorylation site"  
FT 17..169 /note= "mature protein"  
FT 18..20 "calcium phosphorylation site"  
FT 29..32 /note= "cAMP protein kinase phosphorylation site"  
FT 29 /note= "phosphorylation site"  
FT 31 /note= "phosphorylation site"  
FT 49..51 /note= "protein kinase C phosphorylation site"  
FT 51 /note= "phosphorylation site"  
FT 53 /note= "phosphorylation site"  
FT 53..55 /note= "calcium phosphorylation site"  
FT 61 /note= "phosphorylation site"  
FT 61..64 /note= "cAMP protein kinase phosphorylation site"  
FT 64 /note= "phosphorylation site"  
FT 67..69 /note= "calcium phosphorylation site"  
FT 112..114 /note= "N-glycosylation site"  
FT 123..127 /note= "myristoylation site"  
FT 127..129 /note= "protein kinase C phosphorylation site"  
FT 139 /note= "phosphorylation site"  
FT 141 /note= "phosphorylation site"

WO200042187-A1.

20-JUL-2000.

10-JAN-2000; 2000WO-US000005.

11-JAN-1999; 99US-0229402.

(SCHE ) SCHERING CORP.

Gorman DM, Bazan JF, Kastelein RA;

WPI; 2000-476060/41.

N-PSDB; AAA59160.

New DNA sequence encoding a mammalian homolog of CTLA-8, designated  
interleukin-171 (IL-171), useful for recombinant production of IL-171  
which can be used for treating conditions associated with abnormal  
physiology or development -

Disclosure; Page 21; 11lpp; English.

The present sequence represents an interleukin (IL)-174 polypeptide.  
It is a mammalian homologue of the cytokine designated CTLA-8 (also  
referred to as IL-17). The specification also describes homologues  
IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA  
sequence encoding IL-171 is useful for identifying genes, mRNA and  
cDNA molecules which code for related or homologous proteins. The

CC IL-171 protein, antibodies against IL-171, and compounds which have  
CC binding affinity to IL-171 are useful in treatment of conditions  
CC associated with abnormal physiology or development, including abnormal  
CC proliferation, e.g. cancerous conditions, or degenerative conditions.  
CC The IL-171 protein can be used in kits and assay methods for identifying  
CC compounds that selectively bind to IL-171.

XX  
SQ Sequence 169 AA;  
Query Match 77.9%; Score 709; DB 21; Length 169;  
Best Local Similarity 76.8%; Pred. No. 2.7e-65;  
Matches 129; Conservative 9; Mismatches 22; Indels 8; Gaps 1;  
QY 1 MYQVAFAMVGMGTHY-----SHWSPCCPSKGGDTSEELLRWSTVPPPLEPARPN 52  
DB 1 MYQVAFAMVGMGTHYVSLRIQEGCSHLPSCCPKSGKEPPEWLKWSASVSPPELSHT 60  
QY 53 RHPECRASEDGPLNSRAISPMRYELDRDLNRPQDLYHARCLCPHCVSLQTSMDPRG 112  
DB 61 HHAESCRASKDGPLNSRAISPMRYELDRDLNRPQDLYHARCLCPHCVSLQTSMDPLG 120  
QY 113 NSELLYHNOTVYRRPCHGCKGTHKGYCLERLRYRSLACVCVPRVM 160  
DB 121 NSVPLYHNOTVYRRPCHGEGTHRRYCLERLRYRSLACVCVPRVM 168

RESULT 12  
AAE18121  
ID AAE18121 standard; Protein; 169 AA.

XX  
AC AAE18121;  
XX  
DT 07-MAY-2002 (first entry)  
XX  
DE Mouse Interleukin-17 like (IL-17L) protein.

XX  
KW Mouse; interleukin-17 like; IL-17L; immune system dysfunction; diabetes;  
KW cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;  
KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;  
KW autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;  
KW infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;  
KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;  
KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;  
KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;  
KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;  
cancer.

XX  
OS Mus musculus.

XX  
FH Key Location/Qualifiers  
FT Peptide 1..18  
FT Protein /label= Signal\_peptide  
FT Protein 19..169  
FT Protein /label= Mature\_IL\_17L\_protein

XX  
PN WO200208285-A2.

XX  
PD 31-JAN-2002.

XX  
PF 21-JUN-2001; 2001WO-US19861.

XX  
PR 22-JUN-2000; 2000US-213125P.

XX  
PR 02-FEB-2001; 2001US-266159P.

XX  
PR 16-MAR-2001; 2001US-0810384.

XX  
PA (AMGE-) AMGEN INC.

XX  
PI Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ, Jing S;

XX  
DR WPI; 2002-155217/20.

XX  
DR N-PSDB; AAD28772.

XX  
PT Nucleic acid molecules encoding Interleukin 17 (IL-17) - like

PT polypeptides useful in the treatment, prevention and diagnosis of  
PT diseases e.g. cancer

XX  
PS Claim 13; Fig 2; 242pp; English.

XX  
CC The invention relates to nucleic acid molecules encoding Interleukin 17  
CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels  
CC of IL-17 protein in an animal. The IL-17 protein is useful for treating,  
CC preventing or ameliorating a disease, such as immune system dysfunction  
CC (rheumatoid arthritis, osteoarthritis, inflammatory joint disease),  
CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel  
CC disease, transplant rejection, graft vs. host disease), infections (HIV,  
CC hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,  
CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung  
CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin  
CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone  
CC (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy  
CC atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma  
CC leukaemia); reproductive (infertility, miscarriage, endometriosis), eye  
CC (blindness), retinal neuropathy) and treatment of diseases involving  
CC inflammation. The present sequence is mouse Interleukin-17 like (IL-17L)  
CC protein.

XX  
SQ Sequence 169 AA;

Query Match 77.9%; Score 709; DB 23; Length 169;  
Best Local Similarity 76.8%; Pred. No. 2.7e-65;  
Matches 129; Conservative 9; Mismatches 22; Indels 8; Gaps 1;

QY 1 MYQVAFAMVGMGTHY-----SHWSPCCPSKGGDTSEELLRWSTVPPPLEPARPN 52  
DB 1 MYQVAFAMVGMGTHYVSLRIQEGCSHLPSCCPKSGKEPPEWLKWSASVSPPELSHT 60

QY 53 RHPECRASEDGPLNSRAISPMRYELDRDLNRPQDLYHARCLCPHCVSLQTSMDPRG 112  
DB 61 HHAESCRASKDGPLNSRAISPMRYELDRDLNRPQDLYHARCLCPHCVSLQTSMDPLG 120

QY 113 NSELLYHNOTVYRRPCHGCKGTHKGYCLERLRYRSLACVCVPRVM 160  
DB 121 NSVPLYHNOTVYRRPCHGEGTHRRYCLERLRYRSLACVCVPRVM 168

RESULT 13

AA52692  
ID AA52692 standard; Protein; 169 AA.

XX  
AC AA52692;

XX  
DT 26-FEB-2002 (first entry)

XX  
DE Murine interleukin 174 (IL-174).

XX  
KW Mouse; murine; interleukin 174; IL-174; cytokine; Th2 response;  
KW innate immune response; inflammation; gut cell growth;  
KW extramedullary haematopoiesis; antibody response; granuloma formation;  
KW autoimmune condition; multiple sclerosis; systemic lupus erythematosus;  
KW rheumatoid arthritis; diabetes; psoriasis; infectious agent;  
KW inflammatory condition; Crohn's disease; ulcerative colitis;  
KW pancreatitis; hepatitis; allergy; Th2-mediated condition;  
KW systemic anaphylactic response; skin hypersensitivity response;  
KW dermatitis; asthma; fibrosis; eosinophilic gastritis; immunomodulator;  
KW antiinflammatory; antiarthritic; antidiabetic; antifungal;  
KW dermatological; neuroprotective; antiallergic; agonist; antagonist.

XX  
OS Mus sp.

XX  
FH Key Location/Qualifiers  
FT Peptide 1..16  
FT Protein /label= Signal\_peptide  
FT Protein 17..169  
FT Protein /label= Mature\_IL-174

XX  
PN WO200179288-A2.

XX PD 25-OCT-2001.  
XX PF 17-APR-2001; 2001WO-US12493.  
XX PR 18-APR-2000; 2000US-198488P.  
XX PA (SCHE) SCHERING CORP.  
XX PI Hurst SD, Zurawski SM, Rennick DM;  
XX DR WPI; 2002-034343/04.  
XX DR N-PSDB; ABA02394.  
XX PT Administering an interleukin 174 agonist or antagonist to a mammal  
XX PT regulates various immune and inflammatory responses and is useful to  
XX PT treat for example autoimmune diseases, allergies or response to an  
XX PT infection  
XX PS Examples; Page 29; 29pp; English.  
XX CC The invention relates to methods of directing an immune response in a  
XX CC mammal by the administration of an agonist or antagonist of the cytokine  
XX CC interleukin 174 (IL-174). Administration of an IL-174 agonist directs the  
XX CC immune response towards a Th2 response, stimulates an innate immune  
XX CC response, augments the inflammatory response from epithelial or  
XX CC fibroblast cells, induces gut cell growth, promotes extramedullary  
XX CC haematopoiesis, or augments an antibody response in serum and faecal  
XX CC material, while administration of an IL-174 antagonist directs the immune  
XX CC response away from a Th2 type response, and prevents inflammation or  
XX CC granuloma formation. IL-174 agonists may be used to treat autoimmune  
XX CC conditions (particularly multiple sclerosis, systemic lupus  
XX CC erythematosus, rheumatoid arthritis, diabetes or psoriasis), a response  
XX CC to an infectious agent, or inflammatory conditions such as Crohn's  
XX CC disease, ulcerative colitis, pancreatitis, or hepatitis. IL-174  
XX CC antagonists may be used to treat inflammatory, allergic or Th2-mediated  
XX CC conditions (e.g., systemic anaphylactic response, skin hypersensitivity  
XX CC response, dermatitis, asthma, fibrosis, or eosinophilic gastritis). The  
XX CC present sequence represents murine IL-174.  
XX CC  
XX CC Sequence 169 AA;  
Query Match 77.9%; Score 709; DB 23; Length 169;  
Best Local Similarity 76.8%; Pred. No. 2.7e-65;  
Matches 129; Conservative 9; Mismatches 22; Indels 8; Gaps 1;  
QY 1 MYQVAVFLAMVGTHTY-----SHWPCPCSKGQDTSEELLRWSTVPPLEPARN 52  
DB 1 MYQVAVFLAMVGTHTVSLRTOEGCSHLPPCCPSKEQEPPEEWLKWSSASVSPPEPLSHT 60  
QY 53 RHPECSRASEDGPLNSRAISPWRVYELDRDLNRLPDLYHARCLPCHVCSLQGTSHMDPRG 112  
DB 61 HHAESCRASKDGPLNSRAISPWSYELDRDLNRPQDLYHARCLPCHVCSLQGTSHMDPLG 120  
QY 113 NSellyHNOTVYRRPCHGEKTHGYCLERLRYVSLACVCRPRVM 160  
DB 121 NSVPLYHNQTVYRRPCHGEKTHRRYCLERLRYVSLACVCRPRVM 168  
RESULT 14  
AAE18122  
ID AAE18122 standard; Protein: 160 AA.  
XX AC AAE18122;  
XX DT 07-MAY-2002 (first entry)  
XX DE Mouse non-secreted form of Interleukin-17 like (IL-17L) protein.  
XX KW Mouse; interleukin-17 like; IL-17L; immune system dysfunction; diabetes;  
XX KW cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;  
XX KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;  
XX KW autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;

KW infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;  
KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;  
KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;  
KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;  
KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;  
XX cancer.  
XX OS Mus musculus.  
XX PN WO200208285-A2.  
XX PD 31-JAN-2002.  
XX PF 21-JUN-2001; 2001WO-US19861.  
XX PR 22-JUN-2000; 2000US-213125P.  
XX PR 02-FEB-2001; 2001US-266159P.  
XX PR 16-MAR-2001; 2001US-0810384.  
XX PA (AMGE-) AMGEN INC.  
XX PI Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HO, Jing S;  
XX WPI; 2002-155217/20.  
XX DR N-PSDB; AAD28773.  
XX PT Nucleic acid molecules encoding Interleukin 17 (IL-17) - like  
XX PT polypeptides useful in the treatment, prevention and diagnosis of  
XX PT diseases e.g. cancer  
XX PS Claim 13; Fig 2; 242pp; English.  
XX CC The invention relates to nucleic acid molecules encoding Interleukin 17  
XX CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels  
XX CC of IL-17 protein in an animal. The IL-17 protein is useful for treating,  
XX CC preventing or ameliorating a disease, such as immune system dysfunction  
XX CC (rheumatoid arthritis, osteoarthritis, inflammatory joint disease);  
XX CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel  
XX CC disease, transplant rejection, graft vs. host disease); infections (HIV,  
XX CC hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,  
XX CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung  
XX CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin  
XX CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone  
XX CC (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy  
XX CC atherosclerosis, heart failure, angiogenesis); tumours, cancers (lymphoma  
XX CC leukaemia); reproductive (infertility, miscarriage, endometriosis), eye  
XX CC (blindness, retinal neuropathy) and treatment of diseases involving  
XX CC inflammation. The present sequence is non-secreted form of mouse  
XX CC Interleukin-17 like (IL-17L) cDNA.  
XX CC Note: The present sequence also shown in sequence listing of the  
XX CC specification lacks a residue at the C terminal end.  
XX CC  
XX CC Sequence 160 AA;  
Query Match 73.6%; Score 670; DB 23; Length 160;  
Best Local Similarity 76.1%; Pred. No. 2.7e-61;  
Matches 121; Conservative 9; Mismatches 21; Indels 8; Gaps 1;  
QY 10 MYWGTHTY-----SHWPCPCSKGQDTSEELLRWSTVPPLEPARNHPESCRA 61  
DB 1 MIWGTHTVSLRTOEGCSHLPPCCPSKEQEPPEEWLKWSSASVSPPEPLSTHTHAESCRAS 60  
QY 62 EDGPLNSRAISPWRVYELDRDLNRLPDLYHARCLPCHVCSLQGTSHMDPRGNSellyHNQ 121  
DB 61 KDGPLNSRAISPWSYELDRDLNRPQDLYHARCLPCHVCSLQGTSHMDPLGNSVPLYHNQ 120  
QY 122 TVFYRRPCHGEKTHGYCLERLRYVSLACVCRPRVM 160  
DB 121 TVFYRRPCHGEKTHRRYCLERLRYVSLACVCRPRVM 159  
RESULT 15  
AAB07599



Search completed: May 12, 2003, 01:59:02  
Job time : 45 secs

GenCore version 5.1.4.p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2003, 00:49:29 ; Search time 1520 Seconds  
(without alignments)  
12330.399 Million cell updates/sec

Title: US-10-037-591A-1  
Perfect score: 644  
Sequence: 1 ctcaagtcactccctcaaaaa.....ggccccggtgatgggctag 644

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description |
|------------|-------|-------------|--------|----------|-------------|
| 1          | 644   | 100.0       | 644    | AX253225 | Sequence    |
| 2          | 644   | 100.0       | 644    | AX365242 | Sequence    |
| 3          | 493   | 76.6        | 504    | AX299773 | Sequence    |
| 4          | 478.4 | 74.3        | 1320   | AX092424 | Sequence    |
| 5          | 478.4 | 74.3        | 1320   | AX164145 | Sequence    |
| 6          | 478.4 | 74.3        | 1320   | AX180768 | Sequence    |
| 7          | 478.4 | 74.3        | 1335   | AF305200 | Homo sapi   |
| 8          | 478   | 74.2        | 486    | AF458059 | Homo sapi   |
| 9          | 336.8 | 52.3        | 1013   | AX365244 | Sequence    |
| 10         | 336.2 | 52.2        | 1496   | AX365250 | Sequence    |
| 11         | 335.2 | 52.0        | 985    | AX299775 | Sequence    |
| 12         | 335.2 | 52.0        | 985    | AF458060 | Sequence    |
| 13         | 327   | 50.8        | 462    | AY034088 | Mus muscu   |
| 14         | 256   | 39.8        | 157910 | CNS01DTR | Human chr   |
| 15         | 256   | 39.8        | 196292 | CNS0000B | Human chr   |
| 16         | 196.8 | 30.6        | 145762 | AC130940 | Rattus no   |
| 17         | 196.8 | 30.6        | 160950 | AC119293 | Rattus no   |
| 18         | 140.2 | 21.8        | 170032 | AC116673 | Mus muscu   |
| 19         | 121   | 18.8        | 160950 | AC119293 | Rattus no   |
| 20         | 121   | 18.8        | 171821 | AC115371 | Rattus no   |
| 21         | 53.8  | 8.4         | 591    | AX427978 | Sequence    |
| 22         | 53.8  | 8.4         | 1047   | AX180766 | Sequence    |
| 23         | 53.8  | 8.4         | 1047   | AX376380 | Sequence    |
| 24         | 53.8  | 8.4         | 1047   | AF152099 | Homo sapi   |
| 25         | 53.8  | 8.4         | 1078   | AF142410 | Homo sapi   |
| 26         | 53.8  | 8.4         | 1177   | AX223949 | Sequence    |
| 27         | 47.8  | 7.4         | 585    | AF458061 | Mus muscu   |
| 28         | 47.6  | 7.4         | 125020 | AF429315 | Homo sapi   |
| 29         | 45.8  | 7.1         | 214572 | AL450341 | Mouse DNA   |
| 30         | 45    | 7.0         | 45     | AX180787 | Sequence    |
| 31         | 44.8  | 7.0         | 153500 | AC128380 | Rattus no   |
| 32         | 43.6  | 6.8         | 125020 | AF429315 | Homo sapi   |
| 33         | 42.8  | 6.6         | 183900 | AC102499 | Mus muscu   |
| 34         | 42.4  | 6.6         | 241087 | AF480884 | Chimpanze   |
| 35         | 42    | 6.5         | 10732  | E32986   | Gene encodi |
| 36         | 41.8  | 6.5         | 92607  | AL583807 | Human DNA   |
| 37         | 41.4  | 6.4         | 884    | AF218727 | Homo sapi   |
| 38         | 41.4  | 6.4         | 687    | AX047648 | Sequence    |
| 39         | 41.4  | 6.4         | 687    | AX055448 | Sequence    |
| 40         | 41.4  | 6.4         | 687    | AX180764 | Sequence    |
| 41         | 41.4  | 6.4         | 687    | AX464312 | Sequence    |
| 42         | 41.4  | 6.4         | 687    | AF152098 | Homo sapi   |
| 43         | 41.4  | 6.4         | 688    | AF184969 | Homo sapi   |
| 44         | 41.4  | 6.4         | 703    | AF110385 | Homo sapi   |
| 45         | 41.4  | 6.4         | 711    | AF212311 | Homo sapi   |

ALIGNMENTS

RESULT 1  
AX253225  
LOCUS AX253225 644 bp DNA linear PAT 05-OCT-2001  
DEFINITION Sequence 22 from Patent WO0168705.  
ACCESSION AX253225  
VERSION AX253225.1 GI:15986362  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 644)  
AUTHORS Jing,S., Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S. and  
Nguyen,H.O.  
TITLE IL-17 receptor like molecules and uses thereof





|                                                                                                                                                                                                                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                               |                                               |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------|-----------------------------------------------|
| <p> <b>VERSION</b><br/> <b>KEYWORDS</b><br/> <b>SOURCE</b><br/> <b>ORGANISM</b><br/> <b>REFERENCE</b><br/> <b>AUTHORS</b><br/> <b>TITLE</b><br/> <b>JOURNAL</b><br/> <b>FEATURES</b><br/> <b>BASE COUNT</b><br/> <b>ORIGIN</b> </p> | <p> AX164145.1 GI:14545087<br/> human.<br/> Homo sapiens<br/> Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br/> Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.<br/> 1 (bases 1 to 1320)<br/> Fong, S., Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L.,<br/> Hillan, K.J., Tamas, D., Watanabe, C.K., Wood, W.I. and Zhang, Z.<br/> Compositions and methods for the treatment of immune related<br/> diseases<br/> Patent: WO 0140465-A 17 07-JUN-2001;<br/> Genentech, Inc. (US)<br/> Location/Qualifiers<br/> 1..1320<br/> /organism="Homo sapiens"<br/> /db_xref="taxon:9606"<br/> 280 a 353 c 384 g 303 t<br/> Query Match 74.3%; Score 478.4; DB 6; Length 1320;<br/> Best Local Similarity 99.8%; Pred. No. 6.6e-108;<br/> Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0; </p> | <p> <b>BASE COUNT</b><br/> <b>ORIGIN</b> </p> | <p> <b>BASE COUNT</b><br/> <b>ORIGIN</b> </p> |
| <p> <b>VERSION</b><br/> <b>KEYWORDS</b><br/> <b>SOURCE</b><br/> <b>ORGANISM</b><br/> <b>REFERENCE</b><br/> <b>AUTHORS</b><br/> <b>TITLE</b><br/> <b>JOURNAL</b><br/> <b>FEATURES</b><br/> <b>BASE COUNT</b><br/> <b>ORIGIN</b> </p> | <p> AX164145.1 GI:14545087<br/> human.<br/> Homo sapiens<br/> Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br/> Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.<br/> 1 (bases 1 to 1320)<br/> Fong, S., Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L.,<br/> Hillan, K.J., Tamas, D., Watanabe, C.K., Wood, W.I. and Zhang, Z.<br/> Compositions and methods for the treatment of immune related<br/> diseases<br/> Patent: WO 0140465-A 17 07-JUN-2001;<br/> Genentech, Inc. (US)<br/> Location/Qualifiers<br/> 1..1320<br/> /organism="Homo sapiens"<br/> /db_xref="taxon:9606"<br/> 280 a 353 c 384 g 303 t<br/> Query Match 74.3%; Score 478.4; DB 6; Length 1320;<br/> Best Local Similarity 99.8%; Pred. No. 6.6e-108;<br/> Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0; </p> | <p> <b>BASE COUNT</b><br/> <b>ORIGIN</b> </p> | <p> <b>BASE COUNT</b><br/> <b>ORIGIN</b> </p> |
| <p> <b>VERSION</b><br/> <b>KEYWORDS</b><br/> <b>SOURCE</b><br/> <b>ORGANISM</b><br/> <b>REFERENCE</b><br/> <b>AUTHORS</b><br/> <b>TITLE</b><br/> <b>JOURNAL</b><br/> <b>FEATURES</b><br/> <b>BASE COUNT</b><br/> <b>ORIGIN</b> </p> | <p> AX164145.1 GI:14545087<br/> human.<br/> Homo sapiens<br/> Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br/> Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.<br/> 1 (bases 1 to 1320)<br/> Fong, S., Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L.,<br/> Hillan, K.J., Tamas, D., Watanabe, C.K., Wood, W.I. and Zhang, Z.<br/> Compositions and methods for the treatment of immune related<br/> diseases<br/> Patent: WO 0140465-A 17 07-JUN-2001;<br/> Genentech, Inc. (US)<br/> Location/Qualifiers<br/> 1..1320<br/> /organism="Homo sapiens"<br/> /db_xref="taxon:9606"<br/> 280 a 353 c 384 g 303 t<br/> Query Match 74.3%; Score 478.4; DB 6; Length 1320;<br/> Best Local Similarity 99.8%; Pred. No. 6.6e-108;<br/> Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0; </p> | <p> <b>BASE COUNT</b><br/> <b>ORIGIN</b> </p> | <p> <b>BASE COUNT</b><br/> <b>ORIGIN</b> </p> |
| <p> <b>VERSION</b><br/> <b>KEYWORDS</b><br/> <b>SOURCE</b><br/> <b>ORGANISM</b><br/> <b>REFERENCE</b><br/> <b>AUTHORS</b><br/> <b>TITLE</b><br/> <b>JOURNAL</b><br/> <b>FEATURES</b><br/> <b>BASE COUNT</b><br/> <b>ORIGIN</b> </p> | <p> AX164145.1 GI:14545087<br/> human.<br/> Homo sapiens<br/> Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br/> Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.<br/> 1 (bases 1 to 1320)<br/> Fong, S., Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L.,<br/> Hillan, K.J., Tamas, D., Watanabe, C.K., Wood, W.I. and Zhang, Z.<br/> Compositions and methods for the treatment of immune related<br/> diseases<br/> Patent: WO 0140465-A 17 07-JUN-2001;<br/> Genentech, Inc. (US)<br/> Location/Qualifiers<br/> 1..1320<br/> /organism="Homo sapiens"<br/> /db_xref="taxon:9606"<br/> 280 a 353 c 384 g 303 t<br/> Query Match 74.3%; Score 478.4; DB 6; Length 1320;<br/> Best Local Similarity 99.8%; Pred. No. 6.6e-108;<br/> Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0; </p> | <p> <b>BASE COUNT</b><br/> <b>ORIGIN</b> </p> | <p> <b>BASE COUNT</b><br/> <b>ORIGIN</b> </p> |



Db 481 GCTGTGTGCGGCCCGGGCTCATGGCTAG 510

RESULT 10  
AX365250  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
CDS

AX365250  
Sequence 9 from Patent WO0208285.  
AX365250  
AX365250.1 GI:18696999  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Medlock, E., Yeh, R., Silbiger, S.M., Elliot, G.S., Nguyen, H.Q. and  
Jing, S.  
11-17 molecules and uses thereof  
Patent: WO 0208285-A 9 31-JAN-2002;  
Angen, Inc. (US)  
Location/Qualifiers  
1. .1496  
/organism="Mus musculus"  
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511..>987  
/note="unnamed protein product"  
/codon\_start=1  
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BASE COUNT 347 a 417 g 322 t  
ORIGIN

Query Match 52.2%; Score 336.2; DB 6; Length 1496;  
Best Local Similarity 79.1%; Pred. No. 1.1e-72;  
Matches 423; Conservative 0; Mismatches 88; Indels 24; Gaps 1;

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Qy 194 GGGAAACCCACACCTACAGC-----CACTGGCCCCAGCTGCTG 229  
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Qy 230 CCCAGCAAAAGGGGAGGACACCTCTGAGGAGCTGCTGAGTGGGACACATGTCCTGTGCC 289  
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Qy 290 TCCCTTAGAGCTGCTAGGCCCCAACCCGCCACCCAGAGTCTCTGAGGCCAGTGAAGATGG 349  
Db 639 CCCCCAGAGCTCTGAGGCCACACCCACCGAGAATCTCTGAGGGCCAGCAGGATGG 698  
Qy 350 ACCCTCAACAGCAGGGCCATCTCCCTCTGAGATATAGTGGACAGACTTCAACCG 409  
Db 699 CCCCTCAACAGCAGGGCCATCTCTCTTGGAGTATGAGTGGACAGGGACTTGAATCG 758  
Qy 410 GCTCCCCAGACCTGTACACGCCGCTGCTGTGCCCGCACTCGCTCAGCTACAGAC 469  
Db 759 GGTCCCCAGACCTGTACACGCCGCTGATGCTGTGCCCACTGCTGCTCAGCTACAGAC 818  
Qy 470 AGGCTCCACATGGACCCCGGGCACTCGGAGCTGCTCTACCAACAACAGACTGTCTT 529  
Db 819 AGGCTCCACATGGACCCCGCTGGCACTCCGCTCCCACTTTACCAACAACAGACTGT 878  
Qy 530 CTACCGCGGCCATGCCATGGCGAAGGGCACCCACAAAGGCTACTGCTGGAGCGGAG 589  
Db 879 CTACCGCGGCCATGCCATGGCGAAGGTACCCATCGCGCTACTGCTGGAGCGGAG 938  
Qy 590 GCTGTACCGTGTTCCTTAGCTGTGTGTGCGGCCCGCTGTGATGGGCTAG 644

[illegible]

|            |            |                                                                                                                                                                                                                                                                                                        |                                    |
|------------|------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------|
| QY         | 615        | GTGTTGTGGCGGCCCGCTGTGATGGCGTAG                                                                                                                                                                                                                                                                         | 644                                |
| DB         | 481        | GTGTGTGTGGCGGCCCGCTCATGCTTGA                                                                                                                                                                                                                                                                           | 510                                |
| RESULT 12  |            |                                                                                                                                                                                                                                                                                                        |                                    |
| AF458060   |            |                                                                                                                                                                                                                                                                                                        |                                    |
| LOCUS      | AF458060   | Mus musculus IL25 mRNA, complete cds.                                                                                                                                                                                                                                                                  | 985 bp mRNA linear ROD 15-JAN-2002 |
| DEFINITION | AF458060   |                                                                                                                                                                                                                                                                                                        |                                    |
| ACCESSION  | AF458060.1 | GI:18034677                                                                                                                                                                                                                                                                                            |                                    |
| VERSION    |            |                                                                                                                                                                                                                                                                                                        |                                    |
| KEYWORDS   |            |                                                                                                                                                                                                                                                                                                        |                                    |
| SOURCE     |            | Mus musculus.                                                                                                                                                                                                                                                                                          |                                    |
| ORGANISM   |            | Mus musculus                                                                                                                                                                                                                                                                                           |                                    |
| REFERENCE  |            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.                                                                                                                                                                   |                                    |
| AUTHORS    |            | 1 (bases 1 to 985)<br>Fort,M.M., Cheung,J., Yen,D., Li,J., Zurawski,S.M., Lo,S.,<br>Menon,S.D., Clifford,R., Hunter,B., Lesley,R., Muchamuel,T.,<br>Hurst,S.D., Zurawski,G., Leach,M.W., Gorman,D.M. and Rennick,D.M.<br>IL-25 induces IL-4, IL-5, and IL-13 and Th2-associated pathologies<br>in vivo |                                    |
| TITLE      |            | Immunity 15 (6), 985-995 (2001)                                                                                                                                                                                                                                                                        |                                    |
| JOURNAL    |            | 2 (bases 1 to 985)                                                                                                                                                                                                                                                                                     |                                    |
| MEDLINE    |            | Hurst,S.D., Muchamuel,T., Gorman,D.M., Gilbert,J.M., Clifford,T.,<br>Kwan,S., Menon,S., Seymour,B., Jackson,C., Kung,T., Brieland,J.,<br>Zurawski,S.M., Chapman,R., Zurawski,G. and Coffman,R.L.                                                                                                       |                                    |
| PUBMED     |            | New IL-17 family members promote Th1 or Th2 responses in the lung:<br>In vivo function of the novel cytokine IL-25                                                                                                                                                                                     |                                    |
| AUTHORS    |            | Unpublished                                                                                                                                                                                                                                                                                            |                                    |
| TITLE      |            | 3 (bases 1 to 985)<br>Gilbert,J.M. and Gorman,D.M.                                                                                                                                                                                                                                                     |                                    |
| JOURNAL    |            | Direct Submission                                                                                                                                                                                                                                                                                      |                                    |
| AUTHORS    |            | Submitted (12-DEC-2001) Genomics, DNAX Research Inc., 901<br>California Ave., Palo Alto, CA 94304, USA                                                                                                                                                                                                 |                                    |
| TITLE      |            | Location/Qualifiers                                                                                                                                                                                                                                                                                    |                                    |
| JOURNAL    |            | 1. .985                                                                                                                                                                                                                                                                                                |                                    |
| AUTHORS    |            | /organism="Mus musculus"                                                                                                                                                                                                                                                                               |                                    |
| TITLE      |            | /strain="C57BL/6"                                                                                                                                                                                                                                                                                      |                                    |
| JOURNAL    |            | /db_xref="taxon:10090"                                                                                                                                                                                                                                                                                 |                                    |
| AUTHORS    |            | 1. .510                                                                                                                                                                                                                                                                                                |                                    |
| TITLE      |            | /notes="cytokine"                                                                                                                                                                                                                                                                                      |                                    |
| JOURNAL    |            | /codon_start=1                                                                                                                                                                                                                                                                                         |                                    |
| AUTHORS    |            | /product="Il25"                                                                                                                                                                                                                                                                                        |                                    |
| TITLE      |            | /protein_id="AAL57623.1"                                                                                                                                                                                                                                                                               |                                    |
| JOURNAL    |            | /db_xref="GI:18034678"                                                                                                                                                                                                                                                                                 |                                    |
| AUTHORS    |            | /translation="MYQAVAFAMIVGVTHVLSRIQEGCSHLPSQCPSEQPPEEWL<br>KWSSASVPPEPLSHPHFAESFASKDGPLNSRAISPMVSVELRLNRPVDLYHARC<br>LCPCHSYLOTGSHMDPLGNSVPLYHNQTVFYRPPCHGEBSGTHRRYCLERLLRYSLAC<br>VCVRPRMA"                                                                                                           |                                    |
| TITLE      |            | VCCRPRMA"                                                                                                                                                                                                                                                                                              |                                    |
| JOURNAL    |            | BASE COUNT 199 a 296 c 268 g 222 t                                                                                                                                                                                                                                                                     |                                    |
| AUTHORS    |            | ORIGIN                                                                                                                                                                                                                                                                                                 |                                    |
| TITLE      |            | Query Match 52.0%; Score 335.2; DB 10; Length 985;                                                                                                                                                                                                                                                     |                                    |
| JOURNAL    |            | Best Local Similarity 81.0%; Pred.No. 1.9e+72;                                                                                                                                                                                                                                                         |                                    |
| AUTHORS    |            | Matches 413; Conservative 0; Mismatches 73; Indels 24; Gaps 1;                                                                                                                                                                                                                                         |                                    |
| TITLE      |            | QY 159 ATGTACCAGGTGGTTGCATTCTTTGGCAATGGTCATGGGAACCCACACACTACAGC----- 212                                                                                                                                                                                                                               |                                    |
| JOURNAL    |            |                                                                                                                                                                                                                                                                                                        |                                    |
| AUTHORS    |            | DB 1 ATGTACCAGGCTGTGCTATCTTTGGCAATGATCGTGGAAACCCACACCGTCAGCTTGCGG 60                                                                                                                                                                                                                                   |                                    |
| TITLE      |            |                                                                                                                                                                                                                                                                                                        |                                    |
| JOURNAL    |            | QY 213 -----CACTGGCCCCAGCTGCTGCCCCCAGCAAAGGCGAGCACCTCT 254                                                                                                                                                                                                                                             |                                    |
| AUTHORS    |            |                                                                                                                                                                                                                                                                                                        |                                    |
| TITLE      |            | DB 61 ATCCAGGAGGGCTGCAGTCACTTGCACAGCTGCTGCCCCCAGCAAAGAACACCCCG 120                                                                                                                                                                                                                                     |                                    |
| JOURNAL    |            |                                                                                                                                                                                                                                                                                                        |                                    |
| AUTHORS    |            | QY 255 GAGAGCTGCTGAGGTGGACATGTGCCTGTCCTCCCTAGAGCCTGCTAGSCCCAC 314                                                                                                                                                                                                                                      |                                    |
| TITLE      |            |                                                                                                                                                                                                                                                                                                        |                                    |
| JOURNAL    |            | DB 121 GAGGAGTGGCTGAAGTGGAGCTCTGATCTGTGTCTCCCCCAGAGGCTCTGAGCCACAC 180                                                                                                                                                                                                                                  |                                    |
| TITLE      |            |                                                                                                                                                                                                                                                                                                        |                                    |
| JOURNAL    |            | QY 315 CGCACCCAGAGTCCCTGTAGGCGCACTGAAGATGGAGCCCTCAACAGAGGGGCCATCTCC 374                                                                                                                                                                                                                                |                                    |



[illegible]

|            |                                                            |
|------------|------------------------------------------------------------|
| RESULT 13  |                                                            |
| AY034088   |                                                            |
| LOCUS      | AY034088 462 bp mRNA linear ROD 03-DEC-2001                |
| DEFINITION | Mus musculus interleukin 17E precursor, mRNA, partial cds. |
| ACCESSION  | AY034088                                                   |
| VERSION    | AY034088.1 GI:17266279                                     |

|           |                                                                                                                                                         |
|-----------|---------------------------------------------------------------------------------------------------------------------------------------------------------|
| KEYWORDS  | Mus musculus.                                                                                                                                           |
| SOURCE    | Mus musculus                                                                                                                                            |
| ORGANISM  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 462) |
| REFERENCE | Pan, G., French, D., Mao, W., Maruoka, M., Risser, P., Lee, J., Foster, J., Aggarwal, S., Nicholes, K., Guillet, S., Schow, P. and Gurney, A. L.        |
| AUTHORS   | Forced expression of murine IL-17E induces growth retardation, jaundice, a Th2-biased response, and multiorgan inflammation in mice                     |
| TITLE     |                                                                                                                                                         |

|           |                                                                                                                                                 |                  |       |           |        |
|-----------|-------------------------------------------------------------------------------------------------------------------------------------------------|------------------|-------|-----------|--------|
| JOURNAL   | J. Immunol.                                                                                                                                     | 167              | (11), | 6559-6567 | (2001) |
| MEDLINE   |                                                                                                                                                 | 21571724         |       |           |        |
| PUBMED    |                                                                                                                                                 | 11714825         |       |           |        |
| REFERENCE | 2                                                                                                                                               | (bases 1 to 462) |       |           |        |
| AUTHORS   | Pan, G., Mao, W., Maruoka, M., French, D., Risser, P., Lee, J., Foster, J., Aggarwal, S., Nicholes, K., Guillet, S., Schow, P. and Gurney, A.L. |                  |       |           |        |
| TITLE     | Direct Submission                                                                                                                               |                  |       |           |        |
| - JOURNAL | Submitted (08-MAY-2001)                                                                                                                         |                  |       |           |        |
|           | Molecular Biology, Genentech, 1 DNA Way,                                                                                                        |                  |       |           |        |
|           | South San Francisco, CA 94080, USA                                                                                                              |                  |       |           |        |
| FEATURES  | Location/Qualifiers                                                                                                                             |                  |       |           |        |
| SOURCE    | 1..462                                                                                                                                          |                  |       |           |        |

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/db_xref="GI:17266280"
/translation="VSLRIQEGCSHLPSCCPKSEQPEPWLKWSASVSPPEPLSHT
HAASCRASKDGPLNSRAITSPWEYELDRNLNRPQDLYHARCLCPHCVSQTCGSHMDP
LGNSVPLVHNQTVFYRRPCHGEETHRHYCLERRLYRVSACVCVRPVNA"
1..459
mat_peptide

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|                       |                                      |       |       |      |
|-----------------------|--------------------------------------|-------|-------|------|
| BASE COUNT            | 90 a                                 | 157 c | 130 g | 85 t |
| ORIGIN                | /note="IL-1/B; cytokine"             |       |       |      |
| Query Match           | 50.8%; Score 327; DB 10; Length 462; |       |       |      |
| Best Local Similarity | 84.1%; Pred. No. 2e-70;              |       |       |      |

|         |      |                                                                     |     |            |     |        |    |      |    |
|---------|------|---------------------------------------------------------------------|-----|------------|-----|--------|----|------|----|
| Matches | 369; | Conservative                                                        | 0;  | Mismatches | 70; | Indels | 0; | Gaps | 0; |
| QY      | 206  | CTACAGCCACTGGCCCCAGCTGCTGCCCCCAGCAAAAGCGCAGGACACACCTTCTGAGGAGCTGCCT | 265 |            |     |        |    |      |    |
| Db      | 24   | CTGCAGTGCACTTTGCCAGCTGCTGCCCCCAGCAAAGAGCAAGAACCCTCCGGAGGAGTGGCT     | 83  |            |     |        |    |      |    |
| QY      | 266  | GAGGTGAGACATGTGCTGTGCTTCCTCCCTTAGAGCCCTGTAGGCCCAACCCGACCCACGGA      | 325 |            |     |        |    |      |    |
| Db      | 84   | GAAGTGGAGGCTCTGCATCTCTGTGTCCTCCCTCCAGAGCCCTCTGAGCCACACCCACACGAGGA   | 143 |            |     |        |    |      |    |
| QY      | 326  | GTCTCTGTAGGCCAGTCAAGATGGATGGACCCCTCAACAGCAGGGGCCCATCTCCCCCTGGAGATA  | 385 |            |     |        |    |      |    |
| Db      | 144  | ATCTGTGAGGCCACGACGATGGCCCCCTCAACAGCAGGGCCATCTCTCCTTGAGACTA          | 203 |            |     |        |    |      |    |
| QY      | 386  | TGAGTTGGACAGACATTGAACCGGCTCCGCCAGGACCTGTACACGCGCCCTTGCCTGTGTG       | 445 |            |     |        |    |      |    |
| Db      | 204  | TGAGTTGGACAGGACTTGAATCGGTGCTCCGCCAGGAGCTGTACCCACGCTCGATGCCTGTG      | 263 |            |     |        |    |      |    |
| QY      | 446  | CCGCACCTGGCTAGCCTACAGACAGGCTCCACATGAGACCCCGGGGCAACTCGGAGCT          | 505 |            |     |        |    |      |    |
| Db      | 264  | CCCACATGGGTGAGCCTACAGACAGGCTCCCATGGACCCCTGGGCAACTCCGTCCTC           | 323 |            |     |        |    |      |    |
| QY      | 506  | GCTCTACCAACAACAGACTGTCTTCTTACCGCGGCCATGCCATGCGAGAGGACGCCCA          | 565 |            |     |        |    |      |    |
| Db      | 324  | ACTTTACCAACACAGACGGCTTCTTACCGCGGCCATGCCATGCTGAGGAAGTACCCA           | 383 |            |     |        |    |      |    |
| QY      | 566  | CAAGGGTACTGCTGCGAGCGCAGGCTGTACCGTGTTCCTTACGCTGTGTGTGTGTGCG          | 625 |            |     |        |    |      |    |
| Db      | 384  | TCGCCACTACTGCTTGGAGCGCAGGCTCTACCGAGTCTCCTTGGCTTGTGTGTGTGCG          | 443 |            |     |        |    |      |    |
| QY      | 626  | GCCCCGTGTGATGGGCTAG                                                 | 644 |            |     |        |    |      |    |
| Db      | 444  | GCCCCGGTGCATGGCTTAG                                                 | 462 |            |     |        |    |      |    |

RESULT 14

```
CNSOLDTR      157910 bp   DNA       linear    PRI 28-APR-2001
LOCUS         Human chromosome 14 DNA sequence BAC C-2201G16 of library CalTech-D
DEFINITION    from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION     AL132855
VERSION       AL132855.4 GI:13897280
KEYWORDS      HTG.
SOURCE        human.
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157910)
Hellig,R., Pettit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
Brottier,P., Cattoglio,L., Barbe,V., Pelletier,E., Artiguenave,F.,
Levy,M., Eckenga,R., Bruls,T., Deberardinis,V., Cruaud,C.,
Gapay,G., Saurin,W. and Weissbach,J.
Genotyping of the human chromosome 14
Unpublished
2 (bases 1 to 157910)
Genoscope.
Direct Submission
Submitted (26-APR-2001) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
On Apr 30, 2001 this sequence version replaced gi:12001727.
----- Genome Center
Center: Genoscope / Centre National de Sequençage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: Seqref@genoscope.cns.fr
-----
The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7-end) : R-124D2
Downstream BAC (overlapping the SP6 end) : R-66N24 (AC-AL135999)
----- Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 6.97x in Q20 bases; sum-of-confits
```

```

-----
Overall quality chart :
Range : bases
0 - 26
1 - 9
10 - 19
20 - 29
30 - 39
40 - 49
50 - 59
60 - 69
70 - 79
80 - 89
90 - 99

Percentage of bases with a quality value >= 40 : 99 %
-----
FEATURES
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Location/Qualifiers
1. 157910
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/clone_lib="Caltech-D"
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RHdb:RH92419
dbSTS:STS65422
Identified using the e-PCR software (G. Schuler)"
46758..46857
/note="matching EMBL:N91549
RHdb:RH76320
dbSTS:STS53407
Identified using the e-PCR software (G. Schuler)"
57409..57527
/note="matching EMBL:X52889
RHdb:RH96140
RHdb:RH13799
dbSTS:STS7881
Identified using the e-PCR software (G. Schuler)"
39479 a 37198 c 39593 g 41638 t 2 others

Query Match
Best Local Similarity 39.8% Score 256; DB 9; Length 157910;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 389 GTTGACAGAGACTTGACCGGCTCCCGGAGGAGCTGTACCGGCGGCGTGTGCTGTGCGCC 448
Db 9616 GTTGACAGAGACTTGACCGGCTCCCGGAGGAGCTGTACCGGCGGCGTGTGCTGTGCGCC 9675

Oy 449 GCACTGCTGACCTACAGAGAGCTGCCACATGGACCCCGGGGCACTCGGAGCTGCT 508
Db 9676 GCACTGCTGACCTACAGAGAGCTGCCACATGGACCCCGGGGCACTCGGAGCTGCT 9735

Oy 509 CTACACACAGAGCTGCTTCTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 568
Db 9736 CTACACACAGAGCTGCTTCTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 9795

Oy 569 GGGTACTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 628
Db 9796 GGGTACTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 9855

Oy 629 CCGTGTGATGGGCTAG 644
Db 9856 CCGTGTGATGGGCTAG 9871

RESULT 15
CNS0000B 196292 bp DNA linear PRI 22-MAY-2001
LOCUS Human chromosome 14 DNA sequence BAC R-124D2 of library RPCI-11
DEFINITION Human chromosome 14 of Homo sapiens (Human), complete sequence.
-----
AL049829
AL049829.4 GI:8217859
HTG.
Human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 196292)
Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P.,
Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,
Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C.,
Gyapay, G., Saurin, W. and Weissensbach, J.
Sequencing of the human chromosome 14
Unpublished
2 (bases 1 to 196292)
Genoscope.
Direct Submission
Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage :
Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Jun 3, 2000 this sequence version replaced gi:6138746.
-----
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
-----
The following BAC sequence is oriented from the 17 to the SP6 end.
Upstream BAC (overlapping the 17 end) : R-244E17
Downstream BAC (overlapping the SP6 end) : C-2201G16 (AC=AL132855)
-----
Assembly program: Phrap; version 2.0
Quality coverage: 7.94x in Q20 bases; sum-of-contigs
-----
Overall quality chart :
Range : bases
0 - 9
10 - 19
20 - 29
30 - 39
40 - 49
50 - 59
60 - 69
70 - 79
80 - 89
90 - 99

Percentage of bases with a quality value >= 40 : 99 %
-----
FEATURES
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dbSTS:STS69699
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dbSTS:STS55514
Identified using the e-PCR software (G. Schuler)"
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/note="matching EMBL:R94929  
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dbSTS:STS42930  
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dbSTS:STS20163  
Identified using the e-PCR software (G. Schuler)"  
138568..138647  
/note="matching EMBL:M78986  
RHdb:RH28416  
dbSTS:STS20162  
Identified using the e-PCR software (G. Schuler)"  
138805..138926  
/note="matching EMBL:H72023  
RHdb:RH68657  
dbSTS:STS48564  
Identified using the e-PCR software (G. Schuler)"  
161617..161761  
/note="matching EMBL:AA452257  
RHdb:RH92419  
dbSTS:STS65422  
Identified using the e-PCR software (G. Schuler)"  
194804..194903  
/note="matching EMBL:N91549  
RHdb:RH76320  
dbSTS:STS53407  
Identified using the e-PCR software (G. Schuler)"

BASE COUNT 50870 a 45673 c 47123 g 52626 t  
ORIGIN  
Query Match 39.8%; Score 256; DB 9; Length 196292;  
Best Local Similarity 100.0%; Pred. No. 8.8e-53;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 389 GTTGACAGACCTGACCGGCTCCCGAGGAGCTGACCGCCCGCTGCTGCTGCCC 448  
|||||  
Db 157683 GTTGACAGACCTGACCGGCTCCCGAGGAGCTGACCGCCCGCTGCTGCTGCCC 157742  
|||||  
QY 449 GCACCTGGCTACAGACGCTCCACATGACCGCCCGGCGCAACTCGGAGCTGCT 508  
|||||

Db 157743 GCACCTGGCTACAGACGCTCCACATGACCGCCCGGCGCAACTCGGAGCTGCT 157802  
QY 509 CTACCACAACCACTGTCTTCTACCGCGGCCCATGCCATGGCAGAGGGCACCACAA 568  
|||||  
Db 157803 CTACCACAACCACTGTCTTCTACCGCGGCCCATGCCATGGCAGAGGGCACCACAA 157862  
QY 569 GGGCTACTGCTGAGCGGCGCTGTACCGGTTTCCCTTAGCTTGTGTGTGCGGCC 628  
|||||  
Db 157863 GGGCTACTGCTGAGCGGCGCTGTACCGGTTTCCCTTAGCTTGTGTGTGCGGCC 157922  
QY 629 CCGTGTGATGGGCTAG 644  
|||||  
Db 157923 CCGTGTGATGGGCTAG 157938

Search completed: May 12, 2003, 01:39:15  
Job time : 1650 secs

| Result No. | Score | Query |       | Length | DB                | ID                 | Description |
|------------|-------|-------|-------|--------|-------------------|--------------------|-------------|
|            |       | Match |       |        |                   |                    |             |
| 1          | 36.2  | 5.6   | 12588 | 2      | US-08-387-942C-1  | Sequence 1, Appli  |             |
| C 2        | 35    | 5.4   | 2288  | 4      | US-08-935-433-1   | Sequence 1, Appli  |             |
| C 3        | 35    | 5.4   | 2288  | 4      | US-09-553-133-1   | Sequence 1, Appli  |             |
| C 4        | 35    | 5.4   | 4137  | 4      | US-09-499-964-2   | Sequence 2, Appli  |             |
| C 5        | 34.8  | 5.4   | 1848  | 1      | US-08-447-423-15  | Sequence 15, Appli |             |
| C 6        | 34.8  | 5.4   | 3630  | 3      | US-08-434-000A-5  | Sequence 5, Appli  |             |
| C 7        | 34.8  | 5.4   | 3630  | 4      | US-09-312-157-5   | Sequence 5, Appli  |             |
| C 8        | 34.6  | 5.4   | 3202  | 4      | US-09-287-354-1   | Sequence 1, Appli  |             |
| C 9        | 34.4  | 5.3   | 2033  | 1      | US-08-148-910-14  | Sequence 14, Appli |             |
| C 10       | 34.4  | 5.3   | 2033  | 1      | US-08-448-937A-14 | Sequence 14, Appli |             |
| C 11       | 34.4  | 5.3   | 5392  | 2      | US-08-403-852D-1  | Sequence 1, Appli  |             |
| C 12       | 34.4  | 5.3   | 5392  | 3      | US-08-510-646B-1  | Sequence 1, Appli  |             |
| C 13       | 34.4  | 5.3   | 5392  | 4      | US-09-231-818-1   | Sequence 1, Appli  |             |
| C 14       | 34.2  | 5.3   | 1776  | 1      | US-08-484-840-1   | Sequence 1, Appli  |             |
| C 15       | 34.2  | 5.3   | 1776  | 1      | US-08-483-094-1   | Sequence 1, Appli  |             |
| C 16       | 34.2  | 5.3   | 1776  | 4      | US-09-318-448-13  | Sequence 13, Appli |             |
| C 17       | 34    | 5.3   | 836   | 3      | US-08-674-984-1   | Sequence 1, Appli  |             |
| C 18       | 34    | 5.3   | 836   | 3      | US-08-674-984-2   | Sequence 2, Appli  |             |
| C 19       | 34    | 5.3   | 836   | 5      | PCR-US95-15601-1  | Sequence 2, Appli  |             |
| C 20       | 34    | 5.3   | 836   | 5      | PCR-US95-15601-2  | Sequence 2, Appli  |             |
| C 21       | 33.4  | 5.2   | 813   | 1      | US-08-514-014-11  | Sequence 11, Appli |             |
| C 22       | 33.4  | 5.2   | 813   | 2      | US-08-833-823-11  | Sequence 11, Appli |             |
| C 23       | 33.4  | 5.2   | 813   | 3      | US-09-034-810-1   | Sequence 1, Appli  |             |
| C 24       | 33.4  | 5.2   | 813   | 3      | US-08-685-239-1   | Sequence 1, Appli  |             |
| C 25       | 33.4  | 5.2   | 1505  | 1      | US-07-913-246-1   | Sequence 1, Appli  |             |
| C 26       | 33    | 5.1   | 4267  | 4      | US-08-940-155-51  | Sequence 51, Appli |             |
| C 27       | 33    | 5.1   | 4267  | 4      | US-09-819-964-51  | Sequence 51, Appli |             |

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Matches 77; Conservative 0; Mismatches 70; Indels 0; Gaps 0
QY 146 TGCAGTCCCCAGCATGTACAGGTGGTTGCATTCTTGGCAATGGTCAATGGGAACCCACAC 205
Db 585 TGAAGAGACACCATGCTGACACGATGGAGCTTGGAGTGTGTGGAGCTCTGCACCAAGAC 526
QY 206 CTACAGCCATGGCCCGAGCTGTGCCCCAGCAAGGCGAGGACACCTCTGAGGAGCTGCT 265
Db 525 GGTCAACAGCACCCCGATCACCAGCCCCAACAAAGGGTTGGACATAATAGAGCTGTTGCT 466
QY 266 GAGGTGGAGCACTGTGCTGTGCCTCC 292
Db 465 GAAGACTGTCCTGCCATTTTCTCCTCC 439

RESULT 3
US-09-553-132-1/c
; Sequence 1, Application US/09553132
; Patent No. 6350858
; GENERAL INFORMATION:
; APPLICANT: FEILD, JOHN
; TITLE OF INVENTION: A HUMAN SODIUM DEPENDENT PHOSPHATE
; TITLE OF INVENTION: TRANSPORTER (IPT-1)
; FILE REFERENCE: GH-70006-D1
; CURRENT APPLICATION NUMBER: US/09/553,132
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/044,974
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/935,433
; PRIOR FILING DATE: 1997-09-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2288
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-553-132-1

Query Match 5.4%; Score 35; DB 4; Length 2288;
Best Local Similarity 52.4%; Pred. No. 2.6;
Matches 77; Conservative 0; Mismatches 70; Indels 0; Gaps 0
QY 146 TGCAGTCCCCAGCATGTACAGGTGGTTGCATTCTTGGCAATGGTCAATGGGAACCCACAC 205
Db 585 TGAAGAGACACCATGCTGACAAACGATGGAGCTTGGAGTGTGTGGAGCTCTGCACCAAGAC 526
QY 206 CTACAGCCATGGCCCGAGCTGTGCCCCAGCAAGGCGAGGACACCTCTGAGGAGCTGCT 265
Db 525 GGTCAACAGCACCCCGATCACCAGCCCCAACAAAGGGTTGGACATAATAGAGCTGTTGCT 466
QY 266 GAGGTGGAGCACTGTGCTGTGCCTCC 292
Db 465 GAAGACTGTCCTGCCATTTTCTCCTCC 439

RESULT 4
US-09-499-964-2/c
; Sequence 2, Application US/09499964
; Patent No. 6380374
; GENERAL INFORMATION:
; APPLICANT: Cannon, Paul David
; APPLICANT: Sankuratri, Suryanarayana
; TITLE OF INVENTION: Human Intestinal Npt2B
; FILE REFERENCE: ROCH-001
; CURRENT APPLICATION NUMBER: US/09/499,964
; CURRENT FILING DATE: 2000-02-08
; EARLIER APPLICATION NUMBER: 60/119,321
; EARLIER FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4137
; TYPE: DNA

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Db 1233 TGAGGGAGGCTCTGTGACTGTATCTTGCCCTTACAACTTAAGGATGCCAACAGGCGCA 1292  
QY 325 AGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGCGCATCTCCCTCTGGAGAT 384  
Db 1293 AGTACTGTGTCTACTGGGAAGAGGCTCAAAACGGCCGCTGCCCGCGGCTGGTGGAGAGCC 1352  
QY 385 ATGAGTTGACAGAGACTTGAACCGGCTCCGCCAGGACCTGTACCAAGCCGCTTGGCTGT 444  
Db 1353 GGGGGCTGATGAAGAGCAGTACGAGGCGAGGCTGTGCTCTACCGAGCCGGGCAACG 1412  
QY 445 GCGCGCACTGGCTACGACAGAGGCTCCACATGACACCCCGGGGCAACTCGGAGC 504  
Db 1413 GCACCTACACCGTCTATCTCAACAGCTCACCGATCAGGACGCGCGCTTCTACTGTGCG 1472  
QY 505 TGCTCTACCAAC 518  
Db 1473 TGACCGAGCGGAC 1486

## RESULT 7

US-09-312-157-5  
; Sequence 5, Application US/09312157  
; Patent No. 6303341  
; GENERAL INFORMATION:  
; APPLICANT: ANDREW C. HIATT, JULIAN  
; K.-C. MA, THOMAS LEHNER  
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION  
; PROTEINS IN PLANTS AND THEIR USES

NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/312,157  
FILING DATE: 14-May-1999  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/434,000

ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.  
REGISTRATION NUMBER: 34,613  
REFERENCE/DOCKET NUMBER: 212/127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 552-8400  
TELEFAX: (619) 552-0159  
TELEX: 67-351

## SEQUENCE LISTING

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 3630 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

DESCRIPTION: Bovine Polymunoglobulin Receptor

## FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 152.....2425

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-312-157-5

Query Match 5.4%; Score 34.8; DB 4; Length 3630;  
Best Local Similarity 46.1%; Pred. No. 3.5;  
Matches 117; Conservative 0; Mismatches 137; Indels 0; Gaps 0;  
QY 265 TGAGTTGGACACTGTGCTGTGCTCCCTTAGAGCCTGTAGCCCAACCCGACCCAG 324  
Db 1233 TGAGGGAGGCTCTGTGACTGTATCTTGCCCTTACAACTTAAGATCCCAACAGCGCA 1292  
QY 325 AGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGCGCATCTCCCTCTGGAGAT 384  
Db 1293 AGTACTGTGTCTACTGGGAAGAGGCTCAAAACGGCCGCTGCCCGGCTGGTGGAGAGCC 1352  
QY 385 ATGAGTTGGACAGAGACTTGAACCGGCTCCCGCAGGACCTGTACACCCCGCTTCCCTGT 444  
Db 1353 GGGGGCTGTATGAAGAGCAGTACGAGGCGAGGCTGGTGTCTCTACCCAGGCGGCAACG 1412  
QY 445 GCGCGCACTGGCTACGACAGGCTCCACATGACACCCCGGGGCAACTCGGAGC 504  
Db 1413 GCACCTACACCGTCTATCTCAACAGCTCACCGATCAGGACGCGCGCTTCTACTGTGCG 1472  
QY 505 TGCTCTACCAAC 518  
Db 1473 TGACCGAGCGGAC 1486

## RESULT 8

US-09-287-354-1/c  
; Sequence 1, Application US/09287354  
; Patent No. 6348348  
; GENERAL INFORMATION:  
; APPLICANT: THOMPSON, Catherine C.  
; TITLE OF INVENTION: HUMAN HAIRLESS GENE AND PROTEIN  
; FILE REFERENCE: Thompson-20263/0243435  
; CURRENT APPLICATION NUMBER: US/09/287,354  
; CURRENT FILING DATE: 1999-04-07  
; EARLIER APPLICATION NUMBER: US 60/080,888  
; EARLIER FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 3202  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-287-354-1

Query Match 5.4%; Score 34.6; DB 4; Length 3202;

Best Local Similarity 46.8%; Pred. No. 3.8;

Matches 109; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 354 CTCACAGCAGGGCCATCTCCCTCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTC 413

Db 2838 CTGAGCAGAGAGGGCAGAGGCTCTCAGGGGAGGAGAACTGCTGAGTGACGCTGCTGTCT 2779

QY 414 CCCAGGACCTGTACACGCGCTTGTGCTGTGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCT 473

Db 2778 CACACGCGCTGTACCTGTGTTGGGAGGAGCCCTGTCAGGACACAGCAGCGGCTCTCCGGGGC 2719

QY 474 TCCACATGGACCCCGGGGCAACTCGGAGTGTCTTACCAACACAGAGACTGTCTTCTAC 533

Db 2718 CTGGAGCAGGCTCCAGCAGCTCAGCCCTCTCTCCCGAGGCGCGCGCGGCGCTGCTGCT 2659

QY 534 CGCGGCGCATGCCATGGCGAGAGGCGCACCAAGAGGCTACTGCTGAGGCG 586

Db 2658 ATCCAGGTAGCAGCTGCTGTGGGGCGCCAGGCTCCAGGCGCGCTGCCCGGCG 2606

## RESULT 9

US-08-148-910-14  
; Sequence 14, Application US/08148910  
; Patent No. 5466593  
; GENERAL INFORMATION:  
; APPLICANT: Takeshi SHIMOMURA et al.  
; TITLE OF INVENTION: NO. 5466593el Protein and Gene Encoding Said Protein

NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: 500 kb Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,910
FILING DATE: No. 5466593ember 5, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

```

ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:

```

; INFORMATION FOR SEQ ID NO: 14:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 2033 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: double
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA
;
; ORIGINAL SOURCE:
;
; ORGANISM: human
;
; IMMEDIATE SOURCE:
;
; LIBRARY: Pre-made Lambda phage Library,
;
; LIBRARY: human liver(49, male) cDNA Library (Stratagene)
;
US-08-148-910-14

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RESULT 10  
US-08-448-937A-14  
; Sequence 14, Application US/08448937A  
; Patent No. 5677164  
; GENERAL INFORMATION:  
; APPLICANT: Takeshi SHIMOMURA et al.  
; TITLE OF INVENTION: No. 5677164e1 Protein and Gene Encoding Said Protein  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.

COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch,  
MEDIUM TYPE: 500 Kb Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/448,937A  
FILING DATE: May 24, 1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/148,910  
FILING DATE: No. 5677164ember 5, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
TELEX:

```

% INFORMATION FOR SEQ ID NO: 14:
%   SEQUENCE CHARACTERISTICS:
%     LENGTH: 2033 base pairs
%     TYPE: nucleic acid
%     STRANDEDNESS: double
%     TOPOLOGY: linear
%   MOLECULE TYPE: cDNA
%   ORIGINAL SOURCE:
%     ORGANISM: human
%   IMMEDIATE SOURCE:
%     LIBRARY: Pre-made Lambda phage Library,
%     LIBRARY: human liver(49, male), cDNA Library (Stratagene)
%   US-08-448-937A-14

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US-08-448-937A-14
Query Match
Best Local Similarity 54.8%; Score 34.4; DB 1; Length 2033;
Matches 68; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 434 CCCTGGCTGTGCCGCACTCCGTCAGCCCTACACACAGGCTCCACATGGACCCCGGG 493
Db 915 CAGCTGCTGGCTGGAACTCCGATCTGCTTACGAGAGCTGCACGTGGACTCCGTGG 974
QY 494 CAATCTGGAGTGTCTTACCAACACAGACTGTCTTCTACCGGGGGCCATGCCATGGCGA 553
Db 975 CGCCGGCGCCCTGTGGGCTGGGCCCCCATGCCCTACTCGCGGAATCCGGNCAATGAGA 1034
QY 554 GAAG 557
Db 1035 GAGG 1038

```

```

RESULT 11
US-08-403-852D-1
Sequence 1, Application US/08403852D
Patent No. 5991695
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy Lagard, Valerie
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Biosynthesis
TITLE OF INVENTION: Coding For T
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:

```



ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,852D  
FILING DATE: 10-MAY-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR 93/00923  
FILING DATE: 25-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 92/11441  
FILING DATE: 25-SEP-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03806.0054-00000  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5392 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: S.pristinaespiralis

US-08-403-852D-1

Query Match 5.3%; Score 34.4; DB 2; Length 5392;  
Best Local Similarity 46.6%; Pred. No. 5.2;  
Matches 110; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 277 CTGTGCTGTGCTCCCTAGAGCTGTAGGCGCAACCGCCACAGAGTCTGTAGGG 336  
DB 3478 CTGGGCTGTGCTCCCGCCGAGAGCGCCACGCTCAGCAGCGCTCAGCAGCGCTCGC 3537  
QY 337 CCAGTGAAGATGGACCCCTCAACAGCAGGCGCATCTCCCTCGGAGATATGAGTTGGACA 396  
DB 3538 CCGCTGTCTTCTGGAGAGTCAATGTCGCTGCTTCACTCGGAGTCCGTGACCGAGG 3597  
QY 397 GAGACTGAACGGCTCCCGCCAGGACCTGTACACAGCGCGTTCCTGTGCGCCGACTGCG 456  
DB 3598 GCCACCCGACAGATCGCGGACAGATCAGTGACACCGCTCTCGAGCGCCCTGTGCGCG 3657  
QY 457 TCAGCCTACAGAGAGGCTCCACATGACCGCCCGGCAACTCGGAGTGTCTTAC 512  
DB 3658 AGGACCCCGCTCAGCGCTCGCGGTGAGAGCCCTGTATCACCACCGCGGAGTCCAC 3713

RESULT 12  
US-08-510-646B-1  
Sequence 1, Application US/08510646B  
Patent No. 6077699  
GENERAL INFORMATION:

APPLICANT: Blanc, Veronique  
APPLICANT: Blanche, Francis  
APPLICANT: Crouzet, Joel  
APPLICANT: Jacques, Nathalie  
APPLICANT: Lacroix, Patricia  
APPLICANT: Thibaut, Denis  
APPLICANT: Zagorec, Monique

APPLICANT: Debussche, Laurent  
APPLICANT: De Crecy-Iagard, Valerie  
TITLE OF INVENTION: Polypeptides Involved In The  
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences  
TITLE OF INVENTION: Coding For These Polypeptides And Their Use  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/510,646B  
FILING DATE: 03-AUG-1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/403,852  
FILING DATE: 10-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR 93/00923  
FILING DATE: 25-SEP-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 92/11441  
FILING DATE: 25-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03806.0054-01000  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5392 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: S.pristinaespiralis

US-08-510-646B-1

Query Match 5.3%; Score 34.4; DB 3; Length 5392;  
Best Local Similarity 46.6%; Pred. No. 5.2;  
Matches 110; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 277 CTGTGCTGTGCTCCCTAGAGCTGTAGGCGCAACCGCCACAGAGTCTGTAGGG 336  
DB 3478 CTGGGCTGTGCTCCCGCCGAGAGCGCCACGCTCAGCAGCGCTCAGCAGCGCTCGC 3537  
QY 337 CCAGTGAAGATGGACCCCTCAACAGCAGGCGCATCTCCCTCGGAGATATGAGTTGGACA 396  
DB 3538 CCGCTGTCTTCTGGAGAGTCAATGTCGCTGCTTCACTCGGAGTCCGTGACCGAGG 3597  
QY 397 GAGACTGAACGGCTCCCGCCAGGACCTGTACACAGCGCGTTCCTGTGCGCCGACTGCG 456  
DB 3598 GCCACCCGACAGATCGCGGACAGATCAGTGACACCGCTCTCGAGCGCCCTGTGCGCG 3657  
QY 457 TCAGCCTACAGAGAGGCTCCACATGACCGCCCGGCAACTCGGAGTGTCTTAC 512  
DB 3658 AGGACCCCGCTCAGCGCTCGCGGTGAGAGCCCTGTATCACCACCGCGGAGTCCAC 3713

RESULT 13



Search completed: May 12, 2003, 01:56:36  
Job time : 70 secs

| Result No. | Score | Query |      | Length | DB                | ID | Description       |
|------------|-------|-------|------|--------|-------------------|----|-------------------|
|            |       | Match |      |        |                   |    |                   |
| 1          | 644   | 100.0 | 644  | 10     | US-09-886-404-1   |    | Sequence 1, Appli |
| 2          | 478.4 | 74.3  | 1320 | 9      | US-09-874-503-5   |    | Sequence 5, Appli |
| 3          | 478.4 | 74.3  | 1320 | 9      | US-10-000-157-5   |    | Sequence 5, Appli |
| 4          | 478.4 | 74.3  | 1320 | 9      | US-10-063-547-155 |    | Sequence 155, App |
| 5          | 478.4 | 74.3  | 1320 | 9      | US-09-747-259-5   |    | Sequence 5, Appli |
| 6          | 478.4 | 74.3  | 1320 | 9      | US-10-063-616-155 |    | Sequence 155, App |
| 7          | 478.4 | 74.3  | 1320 | 9      | US-10-063-502-155 |    | Sequence 155, App |
| 8          | 478.4 | 74.3  | 1320 | 9      | US-10-063-518-155 |    | Sequence 155, App |
| 9          | 478.4 | 74.3  | 1320 | 9      | US-10-063-598-155 |    | Sequence 155, App |
| 10         | 478.4 | 74.3  | 1320 | 9      | US-10-227-693-155 |    | Sequence 155, App |
| 11         | 478.4 | 74.3  | 1320 | 9      | US-09-908-827-5   |    | Sequence 5, Appli |
| 12         | 478.4 | 74.3  | 1320 | 9      | US-10-213-181-17  |    | Sequence 17, Appl |
| 13         | 478.4 | 74.3  | 1320 | 9      | US-10-063-567-155 |    | Sequence 155, App |
| 14         | 478.4 | 74.3  | 1320 | 9      | US-10-063-599-155 |    | Sequence 155, App |
| 15         | 478.4 | 74.3  | 1320 | 9      | US-10-212-912-17  |    | Sequence 17, Appl |
| 16         | 478.4 | 74.3  | 1320 | 9      | US-10-213-044-17  |    | Sequence 17, Appl |
| 17         | 478.4 | 74.3  | 1320 | 9      | US-10-063-595-155 |    | Sequence 155, App |
| 18         | 478.4 | 74.3  | 1320 | 12     | US-10-006-867-155 |    | Sequence 155, App |
| 19         | 336.8 | 52.3  | 1013 | 10     | US-09-886-404-3   |    | Sequence 3, Appli |

Qy 61 GAAAAA\*

7



[illegible]

### RESULT 3

```

US-10-000-157-5
; Sequence 5, Application US/100000157
; Publication No. US20020182673A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul L.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovasnik, Melissa.
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381RIC1P4 (US)
; CURRENT APPLICATION NUMBER: US/10/000,157
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/138387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/172096
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 39
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/931836
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-23
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 39

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; SEQ ID NO 5
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-000-157-5

Query Match      74.3%; Score 478.4; DB 9; Length 1320;
Best Local Similarity 99.8%; Pred. No. 3.9e-143;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 165 CAGGTGGTTCATCTTGGCAATGGTCAATGGGAACCCACACCTACAGCCACTGGCCCGAGC 224
Db 313 CAGGTGGTTCATCTTGGCAATGGTCAATGGGAACCCACACCTACAGCCACTGGCCCGAGC 372

QY 225 TGTGCCCCCAGCAAAAGGGCAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCAGTGTGCCT 284
Db 373 TGTGCCCCCAGCAAAAGGGCAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCAGTGTGCCT 432

QY 285 GTGCCTCCCTAGAGCTGCTAGGCCCCAACCGCCACCCAGAGTCTGTAGGGCCAGTGAA 344
Db 433 GTGCCTCCCTAGAGCTGCTAGGCCCCAACCGCCACCCAGAGTCTGTAGGGCCAGTGAA 492

QY 345 GATGGACCCCTCAACAGCAGGGGCCATCTCCCTCTGGAGATATGATGTGGACAGAGCTTG 404
Db 493 GATGGACCCCTCAACAGCAGGGGCCATCTCCCTCTGGAGATATGATGTGGACAGAGCTTG 552

QY 405 AACCGGCTCCCCCAGGACCTGTACACGCGCGTGTGCTGTGCGCGCAGCTGCTGAGCCTA 464
Db 553 AACCGGCTCCCCCAGGACCTGTACACGCGCGTGTGCTGTGCGCGCAGCTGCTGAGCCTA 612

QY 465 CAGACAGGCTCCACATGAGGACCCCGGGGCAACTCGGAGCTGCTTACCAACACAGACT 524
Db 613 CAGACAGGCTCCACATGAGGACCCCGGGGCAACTCGGAGCTGCTTACCAACACAGACT 672

QY 525 GTCTTTACCGGGCGGCATGCCATGGCAGAGGAGGACCCACAGGGCTACTGCTGGAG 584
Db 673 GTCTTTACAGGGCGGCATGCCATGGCAGAGGAGGACCCACAGGGCTACTGCTGGAG 732

QY 585 CGCAGGCTGTACCGTGTTCCTTAGCTGTGTGTGTGCGGCGCCCTGTGTATGGGCTAG 644
Db 733 CGCAGGCTGTACCGTGTTCCTTAGCTGTGTGTGTGCGGCGCCCTGTGTATGGGCTAG 792

RESULT 4
US-10-063-547-155
; Sequence 155, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230RIC1
; CURRENT APPLICATION NUMBER: US/10/063,547
; PRIOR FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 155
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-547-155

Query Match      74.3%; Score 478.4; DB 9; Length 1320;
Best Local Similarity 99.8%; Pred. No. 3.9e-143;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 165 CAGGTGGTTCATCTTGGCAATGGTCAATGGGAACCCACACCTACAGCCACTGGCCCGAGC 224
Db 313 CAGGTGGTTCATCTTGGCAATGGTCAATGGGAACCCACACCTACAGCCACTGGCCCGAGC 372

QY 225 TGTGCCCCCAGCAAAAGGGCAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCAGTGTGCCT 284
Db 373 TGTGCCCCCAGCAAAAGGGCAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCAGTGTGCCT 432

QY 285 GTGCCTCCCTAGAGCTGCTAGGCCCCAACCGCCACCCAGAGTCTGTAGGGCCAGTGAA 344
Db 433 GTGCCTCCCTAGAGCTGCTAGGCCCCAACCGCCACCCAGAGTCTGTAGGGCCAGTGAA 492

QY 345 GATGGACCCCTCAACAGCAGGGGCCATCTCCCTCTGGAGATATGATGTGGACAGAGCTTG 404
Db 493 GATGGACCCCTCAACAGCAGGGGCCATCTCCCTCTGGAGATATGATGTGGACAGAGCTTG 552

QY 405 AACCGGCTCCCCCAGGACCTGTACACGCGCGTGTGCTGTGCGCGCAGCTGCTGAGCCTA 464
Db 553 AACCGGCTCCCCCAGGACCTGTACACGCGCGTGTGCTGTGCGCGCAGCTGCTGAGCCTA 612

QY 465 CAGACAGGCTCCACATGAGGACCCCGGGGCAACTCGGAGCTGCTTACCAACACAGACT 524
Db 613 CAGACAGGCTCCACATGAGGACCCCGGGGCAACTCGGAGCTGCTTACCAACACAGACT 672

QY 525 GTCTTTACCGGGCGGCATGCCATGGCAGAGGAGGACCCACAGGGCTACTGCTGGAG 584
Db 673 GTCTTTACAGGGCGGCATGCCATGGCAGAGGAGGACCCACAGGGCTACTGCTGGAG 732

QY 585 CGCAGGCTGTACCGTGTTCCTTAGCTGTGTGTGTGCGGCGCCCTGTGTATGGGCTAG 644
Db 733 CGCAGGCTGTACCGTGTTCCTTAGCTGTGTGTGTGCGGCGCCCTGTGTATGGGCTAG 792

RESULT 5
US-09-747-259-5
; Sequence 5, Application US/09747259
; Publication No. US20030008815A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007

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RESULT 6  
US-10-063-616-155  
; Sequence 155, Application US/10063616  
; Publication No. US2003001385A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Flivaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.

RESULT 7  
US-10-063-502-155  
Sequence 155, Application US/10063502  
Publication No. US20030023042A1  
GENERAL INFORMATION:  
APPLICANT: Eaton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,502  
CURRENT FILING DATE: 2002-05-01









[illegible]

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Db      733 CGCAGGCTGTACCGTGTTCCTTAGCTTTGTGTGTGGGCCCGTGATGGGCTAG   792
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RESULT 14
US-10-063-599-155
; Sequence 155, Application US/10063599
; Publication No. US20030078387A1

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Mon May 12 08:06:50 2003

APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Hillan, Kenneth  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune  
TITLE OF INVENTION: Related Diseases  
FILE REFERENCE: P3133RIC2  
CURRENT APPLICATION NUMBER: US/10/212,912  
PRIOR FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: US 10/052,594  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: US 60/172,059  
PRIOR FILING DATE: 1999-12-23  
NUMBER OF SEQ ID NOS: 24  
SEQ ID NO 17  
LENGTH: 1320  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-212-912-17

Query Match 74.3%; Score 478.4; DB 9; Length 1320;  
Best Local Similarity 99.8%; Pred. No. 3.9e-143;  
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 165 CAGGTGGTTCATCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGCCCCAGC 224  
DB 313 CAGGTGGTTCATCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGCCCCAGC 372  
QY 225 TGCCTGCCCAAGCAAGGCGAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCT 284  
DB 373 TGCCTGCCCAAGCAAGGCGAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCT 432  
QY 285 GTGCTCCCTTAGAGCTGCTAGGCCCAACCCGCCACCCAGAGTCTCTAGGGCCAGTGAA 344  
DB 433 GTGCTCCCTTAGAGCTGCTAGGCCCAACCCGCCACCCAGAGTCTCTAGGGCCAGTGAA 492  
QY 345 GATGGACCCCTCAACAGCAGGCGCATCTCCCTGGAGATATGAGTTGGACAGAGACTTG 404  
DB 493 GATGGACCCCTCAACAGCAGGCGCATCTCCCTGGAGATATGAGTTGGACAGAGACTTG 552  
QY 405 AACCGGCTCCCGCAGGACCTGTACACGCGCGGTTGCCCTGTGCCGCACTCGCTCAGCCTA 464  
DB 553 AACCGGCTCCCGCAGGACCTGTACACGCGCGGTTGCCCTGTGCCGCACTCGCTCAGCCTA 612  
QY 465 CAGACAGGCTCCACATGGACACCCCGGGGCAACTCGGAGCTGCTCTACACACACCACT 524  
DB 613 CAGACAGGCTCCACATGGACACCCCGGGGCAACTCGGAGCTGCTCTACACACCACT 672  
QY 525 GTCTTACCGCGCGCATGCCATGGGAGAGGACCCACACAGGCGCTACTGCTGGAG 584  
DB 673 GTCTTACAGGGCGCATGCCATGGGAGAGGACCCACACAGGCGCTACTGCTGGAG 732  
QY 585 CGCAGGCTGACCGTGTCTTCTAGCTGTGTGTGTGGGGCCCGCTGTGATGGGCTAG 644  
DB 733 CGCAGGCTGACCGTGTCTTCTAGCTGTGTGTGTGGGGCCCGCTGTGATGGGCTAG 792

Search completed: May 12, 2003, 01:58:04  
Job time : 98 secs

GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: May 12, 2003, 01:56:39 ; Search time 28 Seconds  
(without alignments)  
552.773 Million cell updates/sec

Title: US-10-037-591A-2

Perfect score: 910

Sequence: 1 MYQVAFPLAMVGMGHTYSHW.....ERRLYRSLACVCVRPRVMG 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Match | Length | DB | ID     | Description        |
|------------|-------|-------|--------|----|--------|--------------------|
| 1          | 107   | 11.8  | 162    | 2  | T32515 | hypothetical prote |
| 2          | 92.5  | 10.2  | 151    | 1  | B45351 | immediate-early pr |
| 3          | 91    | 10.0  | 150    | 2  | I49623 | cytotoxic T-lympho |
| 4          | 86    | 9.5   | 147    | 2  | JC4628 | cytotoxic T-lympho |
| 5          | 83    | 9.1   | 1323   | 2  | I78557 | N-methyl-D-asparta |
| 6          | 81.5  | 9.0   | 467    | 2  | A47388 | serine/threonine p |
| 7          | 80.5  | 8.8   | 422    | 1  | A60503 | sperm-binding glyc |
| 8          | 78.5  | 8.6   | 206    | 2  | T25139 | hypothetical prote |
| 9          | 78    | 8.6   | 358    | 1  | JQ0805 | hypothetical prote |
| 10         | 77    | 8.5   | 263    | 2  | T48742 | hydrogenase (EC 1. |
| 11         | 77    | 8.5   | 344    | 1  | S11776 | hypothetical prote |
| 12         | 76.5  | 8.4   | 1323   | 2  | S27224 | hydrogenase (EC 1. |
| 13         | 75.5  | 8.3   | 446    | 2  | G85064 | N-methyl-D-asparta |
| 14         | 75.5  | 8.3   | 898    | 2  | T14764 | hypothetical prote |
| 15         | 75.5  | 8.3   | 1189   | 2  | JC6118 | hypothetical prote |
| 16         | 74.5  | 8.2   | 850    | 2  | S56015 | SH2-containing ino |
| 17         | 74.5  | 8.2   | 892    | 2  | T06818 | gastric mucin MUC5 |
| 18         | 74.5  | 8.2   | 1132   | 2  | J03844 | DNA topoisomerase  |
| 19         | 74.5  | 8.2   | 1373   | 2  | TE0095 | telomerase catalyt |
| 20         | 74.5  | 8.2   | 1612   | 2  | JC5210 | gastric mucin MUC5 |
| 21         | 73.5  | 8.1   | 735    | 2  | I48101 | DNA (cytosine-5-)  |
| 22         | 73    | 8.0   | 482    | 2  | B31795 | ADAM 6 protein pre |
| 23         | 73    | 8.0   | 1840   | 2  | T30250 | collagen alpha 1(X |
| 24         | 73    | 8.0   | 3744   | 2  | A46715 | CT1 protein - mous |
| 25         | 72.5  | 8.0   | 240    | 2  | A39842 | hypothetical prote |
| 26         | 72.5  | 8.0   | 294    | 2  | T34537 | insulin-like growt |
| 27         | 72.5  | 8.0   | 419    | 2  | T19871 | hypothetical prote |
| 28         | 72.5  | 8.0   | 602    | 2  | H70796 | hypothetical prote |
| 29         | 72.5  | 8.0   | 1188   | 2  | JC4889 | phosphatidylinosit |

30 72.5 8.0 1254 1 JQ1979 structural polypro  
31 72 7.9 238 2 I48605 insulin-like growt  
32 72 7.9 360 1 S11968 hydrogenase (EC 1.  
33 72 7.9 1348 2 S27812 probable epidermal  
34 72 7.9 1348 2 A43917 probable epidermal  
35 71.5 7.9 166 2 C72734 hypothetical prote  
36 71 7.8 488 2 S13423 stromelysin 3 (EC  
37 71 7.8 564 2 T45866 hypothetical prote  
38 71 7.8 1057 2 T30638 hypothetical prote  
39 70.5 7.7 545 1 A39193 cytochrome ccc pre  
40 70.5 7.7 914 1 JN0550 iodide peroxidase  
41 70.5 7.7 3942 2 T42730 Bassoon protein -  
42 70 7.7 148 2 T21334 hypothetical prote  
43 70 7.7 479 2 AD0845 probable flavoprot  
44 70 7.7 583 1 A41129 radixin - mouse  
45 69.5 7.6 108 2 B69152 polyferredoxin - M

## ALIGNMENTS

## RESULT 1

T32515

hypothetical protein C44B12.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

C:Accession: T32515

R:Tin-Wollam, A.

submitted to the EMBL Data Library, December 1997

A:Description: The sequence of C. elegans cosmid C44B12.

A:Reference number: Z21183

A:Accession: T32515

A:Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-162 &lt;TIN&gt;

A:Cross-references: EMBL:AF036692; PIDN:AAB88329.1; GSPDB:GN00022; CESP:C44B12.6

A:Experimental source: strain Bristol N2; clone C44B12

C:Genetics:

A:Gene: CESP:C44B12.6

A:Map position: 4

A:Introns: 41/3; 95/3; 115/1

## Query Match

Best Local Similarity 11.8%; Score 107; DB 2; Length 162;

Matches 34; Conservative 23; Mismatches 39; Indels 34; Gaps 6;

Qy 27 KGQDTSELLRWSTVPVPPLEPARNRHPESCRAEDGPLNGRAISPPWRYELDRDLNRLP 86

Db 57 KSRDCSEPSIDKSSEVLP-----DQPLSERSCIPYHLLNYDEKRIP 98

Qy 87 QDLYHARCLCPHCVSLQNG-SHMDPRGNSELYHNQTVFYRRPCGKEGKTHKGVCLERL 145

Db 99 AAISEVECCSPH-VKVGIIICPE-----MMYNRMVLFDDSC--DK-----YVERY 143

Qy 146 YRVSLACVCV 155

Db 144 QKVALACVPV 153

## RESULT 2

B45351

immediate-early protein 2 - saimirine herpesvirus 1 (strain 11)

N:Alternate names: hypothetical protein ORF13

C:Species: saimirine herpesvirus 1

A:Note: host Saimiri sclerurus (common squirrel monkey)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Jul-1999

C:Accession: B45351; D36807

R:Nicholas, J.; Smith, E.P.; Coles, L.; Honess, R.

Virology 179, 189-200, 1990

A:Title: Gene expression in cells infected with gammaherpesvirus saimiri: properties

A:Reference number: A45351; MUID:91021021; PMID:1699352

A:Accession: B45351

A:Molecule type: mRNA

C-Accession: JC4628  
R.; Yao, Z.; Timour, M.; Painter, S.; Fanslow, W.; Spriggs, M.  
Gene 168, 223-225, 1996  
A; Title: Complete nucleotide sequence of the mouse CTLA8 gene,  
A; Reference number: JC4628; MUID:96194901; PMID:8654948  
A; Accession: JC4628  
A; Molecule type: DNA  
A; Residues: 1-147 <YAO>  
A; Cross-references: GB:U35108; NID:gl244499; PIDN:AAA93253.1; PID:gl244500  
C; Genetics:  
A; Gene: ctla8  
A; Introns: 69/2  
C; Superfamily: saimiri herpesvirus immediate-early protein 2  
C; Keywords: cytokine; glycoprotein; lymphocyte  
F; 1-14/domain: signal sequence #status predicted <SIG>  
F; 15-147/Product: cytotoxic T-lymphocyte-associated antigen 8 #status predicted <MAT>  
F; 60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.5%; Score 86; DB 2; Length 147;  
Best Local Similarity 27.3%; Pred. No. 0.86;  
Matches 24; Conservative 16; Mismatches 40; Indels 8; Gaps 3;

Qy 68 NSRAIPWRYELDRDLNLKLPDLYHARCLCPHCVSLOTGSHMDPRGNSELLVHNQTVFYRR 127  
::: ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 60 NRSTSPWTLHRNEPDPDRYPVINEAQRCQRCAE--GKLDDHMNSVLIIQQELLVKRE 117  
::: ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Qy 128 PCHGKETHKGVCLERLRYSLACVCV 155  
| : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 118 P-----ESCPTFRVEKML--VGVGCTCV 139  
| : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 5  
I78557  
N-methyl-D-aspartate receptor chain NMDAR2D-2 - rat  
C; Species: Rattus norvegicus (Norway rat)  
C; Date: 02-Aug-1996 #sequence.revision 02-Aug-1996 #text\_change 21-Jan-2000  
C; Accession: I78557; I58158; D45219  
R; Monyer, H.; Burnashev, N.; Laurie, D.J.; Sakmann, B.; Seeburg, P.H.  
Neuron 12, 529-540, 1994  
A; Title: Developmental and regional expression in the rat brain and functional properties of the recombinant NR1 and NR2B subunits of the N-methyl-D-aspartate receptor  
A; Reference number: I58158; MUID:94206533; PMID:7512349  
A; Accession: I78557  
A; Status: preliminary; translated from GB/EMBL/DDBBJ  
A; Molecule type: mRNA  
A; Residues: 1-1323 <RES>  
A; Cross-references: GB:L31612; NID:g469068; PIDN:AAC37647.1; PID:g469069  
A; Accession: I58158  
A; Status: preliminary; translated from GB/EMBL/DDBBJ  
A; Molecule type: mRNA  
A; Residues: 1-66,'V',68-1323 <RE2>  
A; Cross-references: GB:L31611; NID:g469066; PIDN:AAC37646.1; PID:g469067  
R; Ishii, T.; Moriyoshi, K.; Sugihara, H.; Sakurada, K.; Kadotani, H.; Yokoi, M.; Akazawa, Y.  
J. Biol. Chem. 268, 2836-2843, 1993  
A; Title: Molecular characterization of the family of the N-methyl-D-aspartate receptors  
A; Reference number: A45219; MUID:93155102; PMID:8428958  
A; Accession: D45219  
A; Status: preliminary; not compared with conceptual translation  
A; Molecule type: nucleic acid  
A; Residues: 1265-1323 <ISH>  
A; Experimental source: brain  
A; Note: sequence extracted from NCBI backbone (NCBITP:124265)  
C; Superfamily: N-methyl-D-aspartate receptor 2R; glutamate receptor homology  
F; 451-879/Domain: glutamate receptor homology <GRH>

Query Match 9.1%; Score 83; DB 2; Length 1323;  
Best Local Similarity 26.7%; Pred. No. 15;  
Matches 35; Conservative 7; Mismatches 39; Indels 50; Gaps 7;

Qy 38 WSTVPVPLEPAR---PNRHPESCRASDGPL-----NSRAISPWRVELDRDLNLKPQ 87  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 1202 WAAGP-PRRRARCGCPHPHPRPASHRAPAAPAHHRHHRAAGGWDFPPPAFTSRSL 1260  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Qy 88 DL-----YHARCICPHCV-----SLQTGSHMDPRGNSELLVHNQTVFYRR 127

Db 1261 DLSSCPRAAPTRRLTGPSSRHAR-RCPHAAHWGPPPLPTASHRRHRG----- 1304  
QY 128 PCHGEGTHKG 138  
Db 1305 ---GDLGTRRG 1312

## RESULT 6

A47388  
serine/threonine protein kinase - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: A47388  
R:Patricotis, C.; Makris, A.; Bear, S.E.; Tschlis, P.N.  
Proc. Natl. Acad. Sci. U.S.A. 90, 2251-2255, 1993  
A:Title: Tumor progression locus 2 (tpl-2) encodes a protein kinase involved in the prog  
A:Reference number: A47388; MUID:93211939; PMID:7691591  
A:Accession: A47388  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-467 <PAT>  
A:CROSS-references: GB:M4454; NID:g207082; PIDN:AAA42185.1; PID:g207083  
A:Experimental source: liver  
A:Note: sequence extracted from NCBI backbone (NCBIN:128133, NCBI:P:128134)  
C:Superfamily: protein kinase homology  
F:136-388/Domain: protein kinase homology <KIN>

Query Match 9.0%; Score 81.5; DB 2; Length 467;  
Best Local Similarity 30.3%; Pred. No. 7.1;  
Matches 33; Conservative 8; Mismatches 37; Indels 31; Gaps 5;  
QY 24 CPKSGQ--DPSSELLRWSTVPVPLEPAR-----PNRHPESCRAEDGP 65  
Db 50 CPDSNQNKHSESLR-SGQEVPLWSSVRSVGTVEDLLAFANHSNTKHFVRCRQESGI 108  
QY 66 LNSRAISP--WRVELDRDLNRLPDLYHARCLPCHVSLQTSQSHMDPRG 112  
Db 109 LLNMVISPNQGRYQIDSDVLLVPKLYR-----SIGSGFVPRG 147

## RESULT 7

A60503  
sperm-binding glycoprotein ZP3 precursor - golden hamster  
N:Alternate names: sperm receptor; zona pellucida glycoprotein ZP3  
C:Species: Mesocricetus auratus (golden hamster)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A60503  
R:Kinloch, R.A.; Ruiz-Seiler, B.; Wassarman, P.M.  
Dev. Biol. 142, 414-421, 1990  
A:Title: Genomic organization and polypeptide primary structure of zona pellucida glycop  
A:Reference number: A60503; MUID:91078540; PMID:2257975  
A:Accession: A60503  
A:Molecule type: DNA  
A:Residues: 1-422 <KIN>  
A:CROSS-references: GB:M63629  
A:Note: the authors translated the codon CAA for residue 251 as Glu, and AGG for residue  
C:Comment: This sulfated glycoprotein in the zona pellucida of the oocyte is a receptor  
C:Superfamily: sperm-binding glycoprotein ZP3; ZP domain homology  
C:Keywords: glycoprotein; oocyte  
F:45-300/Domain: ZP domain homology <ZPH>

Query Match 8.8%; Score 80.5; DB 1; Length 422;  
Best Local Similarity 29.7%; Pred. No. 7.9;  
Matches 33; Conservative 14; Mismatches 37; Indels 27; Gaps 6;

QY 24 CPKSGQDTSBELLRWSTV-----PVPPLPARPNRH--PESCRASDGLNSRAISPWR 75  
Db 98 CSNRVQVT-EDALVYSIVLLHQRPVPGLSILNTNRADVPICRYPQGNVSSHAIRPTW 156

QY 76 YELDRDLN-----RLPDLYHARCLCP--HC-----VSLQTSQSHM 108  
Db 157 VPFTSTVSSEKLVFLSLRLMEENWNTKLSPTSHLGEVAVLQAEVQVQSHL 207

## RESULT 8

T25139  
hypothetical protein T22H6.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T25139  
R:McMurray, A.  
submitted to the EMBL Data Library, August 1995  
A:Reference number: Z19986  
A:Accession: T25139  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-206 <WIL>  
A:CROSS-references: EMBL:Z50797; PIDN:CAA90671.1; GSPDB:GN00028; CESP:T22H6.1  
A:Experimental source: clone T22H6  
C:Genetics:  
A:Gene: CESP:T22H6.1  
A:Map position: X  
A:Introns: 19/2; 80/3; 128/3; 162/3

Query Match 8.6%; Score 78.5; DB 2; Length 206;  
Best Local Similarity 20.0%; Pred. No. 5.8;  
Matches 33; Conservative 21; Mismatches 46; Indels 65; Gaps 6;  
QY 18 SHWPSCCP-----KQDTSSELLRWSTVPVPLEPARPNRHPESCRA-----S 61  
Db 63 SHYSPAPSYQOALLRLQVGLKHEQITKSS-----GKCNKKLDTIS 106  
QY 62 EDGPLNSRAISPRWYELDRDLNRLPDLYHARCLPCHVSLQTSQSHMDPRGHSSELL---- 117  
Db 107 AETPLDRALCKFEVLNYPKRLPAALTEVKCSC-----PRPNSKLVGKRI 153  
QY 118 -----YHNTVTVRRPCHGEKTHKGYCLERRLYRVSLACV 155  
Db 154 FECEHLRYQVRVLMWDDSCN-----TFREHVETIALACIPV 189

## RESULT 9

JQ0805  
hydrogenase (EC 1.18.99.1) small chain precursor - Azotobacter vinelandii  
N:Alternate names: hydrogenylase; [NiFe]hydrogenase  
C:Species: Azotobacter vinelandii  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 20-Apr-2000  
C:Accession: JQ0805  
R:Menon, A.L.; Stults, L.W.; Robson, R.L.; Mortenson, L.E.  
Gene 96, 67-74, 1990  
A:Title: Cloning, sequencing and characterization of the [NiFe]hydrogenase-encoding s  
A:Reference number: JQ0805; MUID:91092503; PMID:2265761  
A:Molecule type: DNA  
A:Residues: 1-358 <MEN>  
A:CROSS-references: GB:M33152; NID:gl42310; PIDN:AAA82505.1; PID:gl42311  
A:Experimental source: strain OP  
A:Note: part of this sequence, including the amino end of the mature protein, was con  
C:Genetics:  
A:Gene: hoxk  
C:Complex: heterodimer; large and small chain  
C:Function:  
A:Pathway: hydrogen metabolism  
A:Note: contains iron-sulfur and nickel  
C:Superfamily: hydrogenase (NiFe) small chain  
C:Keywords: 3Fe-4S; 4Fe-4S; heterodimer; hydrogen metabolism; iron-sulfur protein; me  
F:1-45/Domain: signal sequence #status predicted <SIG>  
F:46-358/Product: hydrogenase small chain #status experimental <NAT>  
F:62, 65, 160, 194/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F:232, 235, 260, 266/Binding site: 4Fe-4S cluster (His, Cys, Cys) (covalent) (type  
F:275, 294, 297/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 8.6%; Score 78; DB 1; Length 358;  
Best Local Similarity 21.9%; Pred. No. 11;  
Matches 37; Conservative 19; Mismatches 35; Indels 78; Gaps 11;



C;Superfamily: hydrogenase (NiFe) small chain  
C;Keywords: 3Fe-4S; 4Fe-4S; heterodimer; hydrogen metabolism; iron-sulfur protein; m

F;1-34/Domain: signal sequence #status predicted <SIG>  
F;35-344/Product: hydrogenase (uptake) small chain #status predicted <MAT>  
F;51\_54\_146\_180/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F;218\_221\_246\_252/Binding site: 4Fe-4S cluster (His, Ser, Cys, Cys) (covalent) (type  
F;261\_280\_283/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 8.5%; Score 77; DB 1; Length 344;  
Best Local Similarity 21.3%; Pred. No. 13;  
Matches 36; Conservative 21; Mismatches 34; Indels 78; Gaps 11;

QY 20 WPSCCPKGDTSEELLRNSTVPPLEPARPNRHPHPCSCRAEDCPPLNSRAISPRRYELD 79  
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
Db 143 WGSCA-----SWGCV-----QAAPN-----PTQAVPIHKVTID 171  
QY 80 RDLNLRLPODLYHARCLCPHCVSLSQTG-----SHMDPRGNSELLY-----HNQTVF 124  
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
Db 172 KPMKVPG-----CPPIAEVWTGVITYMLTFGLPELDROGRPKMFYGRIHDKS-- 221  
QY 125 YRRPCH-----GEKGTHRGKGLERLRYRVSL-----ACVCVR 156  
Db |||| :|| |||| |||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
Db 222 YRRP-HFDAGQFVEHWDDGARKGYC----LYKVGCKGPTSYNACSTVR 265

RESULT 12  
S27224  
N-methyl-D-aspartate receptor epsilon-4 chain - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 25-Feb-1994 #sequence\_revision 01-Sep-1995 #text\_change 17-Mar-1999  
C;Accession: S27224  
R;Ikeda, K.; Nagasawa, M.; Mori, H.; Araki, K.; Sakimura, K.; Watanabe, M.; Inoue, Y.  
FEBS Lett. 313, 34-38, 1992  
A;Title: Cloning and expression of the epsilon-4 subunit of the NMDA receptor channel  
A;Reference number: S27224; PMID:93050214; PMID:1385220  
A;Accession: S27224  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1323 <IKEX>  
A;Cross-references: EMBL:D12822  
C;Superfamily: N-methyl-D-aspartate receptor 2D; glutamate receptor homology  
C;Keywords: transmembrane protein  
F;451-879/Domain: glutamate receptor homology <GRH>

Query Match 8.4%; Score 76.5; DB 2; Length 1323;  
Best Local Similarity 25.5%; Pred. No. 58;  
Matches 35; Conservative 6; Mismatches 41; Indels 55; Gaps 7;

QY 38 WSTVPVP-----PLEPAR-----PNRHSPCSRAEDGGPL-----NSRAISPRRYELDRD 81  
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
Db 1195 WAPPPPPWAAGPAPRRARGCGPRPHPRASHRAPAAAPHHHRRRAAGGWDLPPAP 1254  
QY 82 LNRLPDLL-----YHARCCLPCHV-----SLTSGSHMDPRGNSELLYHNQ 121  
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
Db 1255 TRSLEDLSCPRAATPRLTGTSPSRHAR-RCPHAHWGCPPLTASRRHRG----- 1304  
QY 122 TVFYRRPCHGEGKTHG 138  
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
Db 1305 -----GDLGTRRG 1312

RESULT 13  
G85064  
hypothetical protein AF4g05150 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
C;Accession: G85064  
R;anonymus, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp  
Nature 402, 769-777, 1999  
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A;Reference number: A85001; PMID:20083488; PMID:10617198  
A;Accession: G85064  
A;Status: preliminary



| Result No. | Score | Query |        | DB ID | Description |
|------------|-------|-------|--------|-------|-------------|
|            |       | Match | Length |       |             |
| 1          | 898   | 98.7  | 177    | 1     | II17E_HUMAN |
| 2          | 165.5 | 18.2  | 197    | 1     | II17C_HUMAN |
| 3          | 125.5 | 13.8  | 180    | 1     | II17B_HUMAN |
| 4          | 123.5 | 13.6  | 180    | 1     | II17B_MOUSE |
| 5          | 120.5 | 13.2  | 153    | 1     | II17F_MOUSE |
| 6          | 116.5 | 12.8  | 178    | 1     | II17B_HUMAN |
| 7          | 96.5  | 10.6  | 155    | 1     | II17B_MESAU |
| 8          | 92.5  | 10.2  | 151    | 1     | II17F_HUMAN |
| 9          | 91    | 10.0  | 150    | 1     | VG13_HSUSA  |
| 10         | 89.5  | 9.8   | 151    | 1     | II17_RAT    |
| 11         | 86    | 9.5   | 158    | 1     | VG13_HSVSC  |
| 12         | 83    | 9.1   | 1323   | 1     | II17_MOUSE  |
| 13         | 81.5  | 9.0   | 467    | 1     | NME4_RAT    |
| 14         | 80.5  | 8.8   | 422    | 1     | M3K8_RAT    |
| 15         | 78    | 8.6   | 358    | 1     | P23_MESAU   |
| 16         | 77.5  | 8.5   | 966    | 1     | MBHS_AZOV1  |
| 17         | 77.5  | 8.5   | 1581   | 1     | ST10_MOUSE  |
| 18         | 77    | 8.5   | 344    | 1     | LMG3_MOUSE  |
| 19         | 77    | 8.5   | 1050   | 1     | MBHS_AZOGH  |
| 20         | 76.5  | 8.4   | 988    | 1     | TLR7_MOUSE  |
| 21         | 76.5  | 8.4   | 1323   | 1     | CHS1_EXODE  |
| 22         | 76.5  | 8.4   | 1696   | 1     | NME4_MOUSE  |
| 23         | 74.5  | 8.2   | 1132   | 1     | PKC5_BRACL  |
| 24         | 74.5  | 8.2   | 1612   | 1     | TERT_HUMAN  |
| 25         | 74    | 8.1   | 1336   | 1     | DMN1_PARLI  |
| 26         | 73    | 8.0   | 482    | 1     | NME4_HUMAN  |
| 27         | 73    | 8.0   | 3744   | 1     | CA1B_RAT    |
| 28         | 72.5  | 8.0   | 240    | 1     | YHP9_YEAST  |
| 29         | 72.5  | 8.0   | 545    | 1     | IPB6_HUMAN  |
| 30         | 72.5  | 8.0   | 930    | 1     | HMWC_DESVH  |
| 31         | 72.5  | 8.0   | 1254   | 1     | SM6C_HUMAN  |
| 32         | 72.5  | 8.0   | 3695   | 1     | POLS_EEVMV  |
| 33         | 72    | 7.9   | 238    | 1     | LMA5_MOUSE  |
|            |       |       |        |       | IPB6_MOUSE  |

```
QY 63 DGPLNSRAISPWRYELDRDLNRLPDYHARCLPCHVCSYLSQTSMDPRGNSSELYHNQT 122
DB 79 DGPLNSRAISPWRYELDRDLNRLPDYHARCLPCHVCSYLSQTSMDPRGNSSELYHNQT 138
QY 123 VFYRPPCHGKGTGKGYCLERLRYRSLVSLACVCRPRVMG 161
DB 139 VFYRPPCHGKGTGKGYCLERLRYRSLVSLACVCRPRVMG 177
RESULT 2
IL17C_HUMAN
ID IL17C_HUMAN STANDARD; PRT: 197 AA.
AC Q9P0M4; Q9HC75;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Interleukin-17 precursor (IL-17C) (Cytokine CX2).
GN IL17C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20105548; PubMed=10639155;
RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,
RA Gurney A.L., Wood W.I.;
RT "Cloning and characterization of IL-17B and IL-17C, two new members
RT of the IL-17 cytokine family.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang W., He L., Wan T., Yuan Z., Cao X.;
RT "A novel human cytokine CX2 with homology to IL-17.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Stimulates the release of tumor necrosis factor alpha
CC and IL-1beta from the monocytic cell line THP-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
CC
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CC
DR EMBL; AF152099; AAF28105.1; -
DR EMBL; AF142410; AAG27921.1; -
DR Genew; HGNC:5983; IL17C.
DR MIM; 604628; -
KW Cytokine; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 197 INTERLEUKIN-17C.
FT DISULFID 129 189 BY SIMILARITY.
FT DISULFID 134 191 BY SIMILARITY.
FT CONFLICT 50 50 H -> R (IN REF. 2).
FT SEQUENCE 197 AA; 21765 MW; BAE0152E18DE7D08 CRC64;
SQ
Query Match 18.2%; Score 165.5; DB 1; Length 197;
Best Local Similarity 29.7%; Pred. No. 7.8e-09;
Matches 52; Conservative 16; Mismatches 37; Gaps 7;
QY 15 HTYSHWSPCCSPKQDTSSEEL-----LRW-STVP---VPPLEPAPRPNRHPS 57
DB 27 HPISHGTTPHYS-----AEELPGQAPPHLLARCAKNGQALPVALVSSLEAASHRGHER 81
QY 58 CRASEDGPL-----NSRAISPWRYELDRDLNRLPDYHARCLPCHVCSYLSQTS 106
DB 82 PSATTQCPVLRPEVLEADTHQRSISPWRYVDTDEDYRYPKLAFAECLRCGCIDARTGR 141
QY 107 HMDPRGNSSELYHNQTVFYRRPCHGKGTGKGYCLERLRYRSLVSLACVCRPR 158
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DB 142 ETAAL-NSVRLQSLVLRRRPCSRDGLPTGAFATHTFIHVPVGTCTVLP 195
RESULT 3
IL17B_HUMAN
ID IL17B_HUMAN STANDARD; PRT: 180 AA.
AC Q9UHF5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-17B precursor (IL-17B) (Cytokine-like protein ZCYT07)
DE (Neuronal interleukin-17 related factor) (Interleukin-20).
GN IL17B OR ZCYT07 OR N1RF OR IL20.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
RA Martinez T., Hoffman R., O'Hara P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20317118; PubMed=10749887;
RA Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.J.,
RA Barber M.C., Wang W., Wathen K., Hodge V., Fisher C.L., Olsen H.,
RA Ruben S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A.,
RA Carrell J.A., Ebner R.;
RT "A novel cytokine receptor-ligand pair. Identification, molecular
RT characterization, and in vivo immunomodulatory activity.";
RL J. Biol. Chem. 275:19167-19176(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20105548; PubMed=10639155;
RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,
RA Gurney A.L., Wood W.I.;
RT "Cloning and characterization of IL-17B and IL-17C, two new members
RT of the IL-17 cytokine family.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E.,
RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;
RT "Identification of a novel IL-17 related factor: demonstration of
RT neuronal expression and evaluation as a candidate for the chromosome
RT 5q-linked form of Charcot-Marie-Tooth disease.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Zhang W., Wang J., Cao X.;
RT "Novel cytokine homology with interleukin-17.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Stimulates the release of tumor necrosis factor alpha
CC and IL-1beta from the monocytic cell line THP-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in adult pancreas, small intestine,
CC prostate, colon mucosal lining, and ovary.
CC -!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
CC
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CC
```

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CC EMBL; AF184969; AAF01318.1; -  
DR EMBL; AF212311; AAF78775.1; -  
DR EMBL; AF152098; AAF28104.1; -  
DR EMBL; AF218727; AAG44136.1; -  
DR EMBL; AF110385; AAG39637.1; -  
DR EMBL; AF386077; AAK60336.1; -  
DR Genew; HGNC:5982; IL17B.  
DR MIM; 604627; -  
KW Cytokine; Glycoprotein; Signal.  
FT SIGNAL 1 20 POTENTIAL.  
FT CHAIN 21 180 INTERLEUKIN-17B.  
FT DISULFID 121 176 BY SIMILARITY.  
FT DISULFID 126 178 BY SIMILARITY.  
FT CARBOHYD 75 75 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 180 AA; 20437 MW; FLB0BC1446D0B14A CRC64;

Query Match 13.88; Score 125.5; DB 1; Length 180;  
Best Local Similarity 33.3%; Pred. No. 4.3e-05;  
Matches 30; Conservative 16; Mismatches 39; Indels 5; Gaps 3;

QY 67 NSRAISPRYELDELNLRLPDLYHARCLPHCVSLQTSQSHMDPRGNSSELYHNQTVFYR 126  
DB 94 NKRSLSPWGYSINHDPSRIPVDLPPEARCLCLGCVNPF--MQEDRSVMVSPVFSQVPVRR 151  
QY 127 RPHGEGKTHKGYCLERLYR-VSLACVCV 155  
DB 152 RLCPPPPT--GPCRQAVMETIAGVCTCI 179

RESULT 4  
IL17B\_MOUSE  
ID IL17B\_MOUSE STANDARD; PRT; 180 AA.  
AC Q90X76; Q99MY3; Q9CTI4;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Interleukin-17B precursor (IL-17B) (Cytokine-like protein ZCYTO7)  
GN (Neuronal interleukin-17 related factor) (Cytokine CX1).  
DN IL17B OR ZCYTO7 OR NIFB.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,  
RA Martinez T., Hoffman R., O'Hara P.,  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E.,  
RA Smith D., Rao L., Whitmore T.E., Gilbert T., Kuestner R.E.;  
RT Identification of a novel IL-17 related factor: demonstration of  
RT neuronal expression and evaluation as a candidate for the chromosome  
RT 5q-linked form of Charcot-Marie-Tooth disease.  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Zhang W., Cao X.;  
RC STRAIN=BALE/C;  
RA Zhang W., Cao X.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Embryo;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Ozawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Qjacksonbush J.,  
Schrini L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boiffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Stimulates the release of tumor necrosis factor alpha  
CC and IL-beta from the monocytic cell line THP-1 (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.

-----  
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CC EMBL; AF184970; AAF01319.1; -  
DR EMBL; AF218726; AAG44135.1; -  
DR EMBL; AF250308; AAK37427.1; -  
DR EMBL; AK003506; BAB22826.1; -  
DR EMBL; BC002271; AAH02271.1; -  
DR MGD; MGI:1928397; Il17b.  
KW Cytokine; Glycoprotein; Signal.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 180 INTERLEUKIN-17B.  
FT DISULFID 121 176 BY SIMILARITY.  
FT DISULFID 126 178 BY SIMILARITY.  
FT CARBOHYD 75 75 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CONFLICT 1 7 MDWPSL -> YPTSTFS (IN REF. 4).  
FT CONFLICT 33 33 G -> R (IN REF. 4).  
FT CONFLICT 34 34 R -> K (IN REF. 3).  
FT CONFLICT 65 65 N -> T (IN REF. 3).  
FT CONFLICT 76 76 S -> I (IN REF. 4).  
SQ SEQUENCE 180 AA; 20309 MW; E26F4C72001997C5 CRC64;

Query Match 13.68; Score 123.5; DB 1; Length 180;  
Best Local Similarity 32.2%; Pred. No. 6.7e-05;  
Matches 29; Conservative 17; Mismatches 39; Indels 5; Gaps 3;

QY 67 NSRAISPRYELDELNLRLPDLYHARCLPHCVSLQTSQSHMDPRGNSSELYHNQTVFYR 126  
DB 94 NKRSLSPWGYSINHDPSRIPVDLPPEARCLCLGCVNPF--MQEDRSVMVSPVFSQVPVRR 151  
QY 127 RPHGEGKTHKGYCLERLYR-VSLACVCV 155  
DB 152 RLC--PQPRPGPCRQVVMETIAGVCTCI 179

RESULT 5  
IL17F\_HUMAN  
ID IL17F\_HUMAN STANDARD; PRT; 153 AA.  
AC Q96PD4; Q9NUE6; Q9GPI8;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Interleukin-17F precursor (IL-17F) (Interleukin-24) (Cytokine ML-1).  
GN IL17F OR IL24.  
OS Homo sapiens (Human).



```

Db      140 VSVGCTCTVPIV 151

||: | || |
RESULT 8
VG13_HSVSA STANDARD; PRT; 151 AA.
AC P24916;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Immediate early gene 13 protein precursor.
GN 13 OR KCLF2.
OS Herpesvirus saimiri (strain 11).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gamaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10383;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90163221; PubMed=2154888;
RY Albrecht J.-C., Fleckenstein B.;
RA "Structural organization of the conserved gene block of Herpesvirus
RT saimiri coding for DNA polymerase, glycoprotein B, and major DNA
RL binding protein.";
RL Virology 174:533-542(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92333688; PubMed=1321287;
RY Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
RA Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
RA Honess R.W.;
RT "Primary structure of the herpesvirus saimiri genome.";
RL J. Virol. 66:5047-5058(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91021021; PubMed=1699352;
RY Nicholas J., Smith E.P., Coles L., Honess R.;
RT "Gene expression in cells infected with gammaherpesvirus saimiri:
RT properties of transcripts from two immediate-early genes.";
RL Virology 179:189-200(1990).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X64346; CAA45636.1; -
DR EMBL; M31122; AAA46169.1; -
DR EMBL; M60286; AAA46136.1; -
DR PIR; D36807; D36807.
DR PIR; B45351; B45351.
DR CytoKine; Early protein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 151 IMMEDIATE EARLY GENE 13 PROTEIN.
FT DISULFID 90 140 BY SIMILARITY.
FT DISULFID 95 142 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 151 AA; 17180 MW; 53BEDDE4206C6432 CRC64;

Query Match 10.2%; Score 92.5; DB 1; Length 151.
Best Local Similarity 27.7%; Pred. No. 0.047;
Matches 31; Conservative 19; Mismatches 43; Indels 19; Gaps 5;

QY 52 NRHPESCRASEDGPLNSRAISPWRYELDRNLNLPDYHARCICPHCVSLQTGSHMDPR 111
| : | |||
DB 51 NWNTSSKRSD--YYNRSTSPWTHRENDODRVPVSYPEAKRCYLGCNVAD----- 99

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CC SPECIES-SPECIFICITY OF THE INSEMINATION.
CC -!- SUBUNIT: ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, IN
CC WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Extracellular
CC matrix.
CC -!- TISSUE SPECIFICITY: OOCYTES.
CC -!- DEVELOPMENTAL STAGE: GROWING OOCYTES.
CC -!- PFM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES.
CC -!- SIMILARITY: CONTAINS 1 ZP DOMAIN.
CC -----
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CC -----
DR EMBL; M63629; AAA37079.1;
DR InterPro; IPR001507; Endoglin/CD105.
DR Pfam; PF00100; zona_pellucida; 1.
DR PRINTS; PR00023; ZPELLUCIDA.
DR SMART; SM00241; ZP; 1.
DR PROSITE; PS00682; ZP_DOMAIN; 1.
KW Glycoprotein; Signal; Sulfation; Sperm; Receptor; Transmembrane;
KW Extracellular matrix.
FT SIGNAL 1 22
FT CHAIN 23 422
FT DOMAIN 23 386
FT TRANSMEM 387 407
FT DOMAIN 408 422
FT DOMAIN 45 306
FT DOMAIN 119 158
FT DOMAIN 208 257
FT CARBOHYD 146 146
FT CARBOHYD 271 271
FT CARBOHYD 302 302
SQ SEQUENCE 422 AA; 45827 MW; D0F95BE7FF8E7E01 CRC64;

Query Match 8.8%; Score 80.5; DB 1; Length 422;
Best Local Similarity 29.7%; Pred. No. 2;
Matches 33; Conservative 14; Mismatches 37; Indels 27; Gaps 6;

QY 24 CPSKGDQTSBELLRWSTV-----VPPLEPARNRH--PESCRASEDGPLNSRAISPWR 75
DQ 98 CSNRVQVT-EDALVYSIVLLHQPVPGLSILRTNRADVPICRPGNVSSHAIRPTW 156
QY 76 YELDRDLN-----RLPDLYHARCLCP--HC-----VSLQTGSHM 108
DQ 157 VPFSTTVSSBEKVLFSRLMEENNTEKLSPTSHLGEVAYLQAEVQTGSHL 207

RESULT 15
MBHS_AZOVI
ID MBHS_AZOVI STANDARD; PRT; 358 AA.
AC P21950;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Uptake hydrogenase small subunit precursor (EC 1.18.99.1)
DE (Hydrogenlyase) (Membrane-bound hydrogenase small subunit)
DE (Hydrogenase beta subunit).
GN HOXK.
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UW;
RX MEDLINE=91092503; PubMed=2265761;
RA Menon A.L., Stults L.W., Robson R.L., Mortenson L.E.;
RT "Cloning, sequencing and characterization of the [Nife]hydrogenase-
```

```
RT encoding structural genes (hoxK and hoxG) from Azotobacter
RT vinelandii."
RL Gene 96:67-74 (1990).
CC -!- FUNCTION: THIS ENZYME RECYCLES THE H(2) PRODUCED BY NITROGENASE TO
CC INCREASE THE PRODUCTION OF ATP AND TO PROTECT NITROGENASE AGAINST
CC INHIBITION OR DAMAGE BY O(2) UNDER CARBON- OR PHOSPHATE-LIMITED
CC CONDITIONS.
CC -!- CATALYTIC ACTIVITY: 2 reduced ferredoxin + 2 H(+) = 2 oxidized
CC ferredoxin + H(2).
CC -!- COFACTOR: CONTAINS NICKEL AND IRON-SULFUR.
CC -!- SUBUNIT: HETEROOLIGOMER OF A LARGE AND A SMALL SUBUNIT.
CC -!- SUBCELLULAR LOCATION: Membrane-bound.
CC -!- SIMILARITY: TO OTHER UPTAKE HYDROGENASES SMALL SUBUNIT.
CC -----
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CC -----
DR EMBL; M33152; AAA82505.1;
DR EMBL; L23970; AAA19498.1;
DR PIR; JQ0805; JQ0805.
DR HSSP; P12943; 1FRV.
DR InterPro; IPR002096; Cmplxl_20kDa.
DR InterPro; IPR001821; Nifehydrog_small.
DR Pfam; PF01058; oxidored_q6; 1.
DR PRINTS; PR00614; NINGNASESMLL.
DR TIGRfams; TIGR00391; hvdA; 1.
KW Oxidoreductase; Signal; Membrane; Iron-sulfur; Nickel.
FT SIGNAL 1 45
FT CHAIN 46 358
FT SEQUENCE 358 AA; 39259 MW; BDCE5646D41D1C23 CRC64;

Query Match 8.6%; Score 78; DB 1; Length 358;
Best Local Similarity 21.9%; Pred. No. 2.9;
Matches 37; Conservative 19; Mismatches 35; Indels 78; Gaps 11;

QY 20 WPSCCPSKQDTSBELLRWSTVPPPPLEPARNRHPPESCRASEDGPLNSRAISPWR 79
DQ 157 WGSCA-----SWGCV-----QAARN-----PTQAVPIHKVITD 185
QY 80 RDLNRLPDQLYHARCLCPHCVSLSQTG-----SHMDPRGNSELY-----HNQTVF 124
DQ 186 KPIVKVPG-----CPPIAEVMVTGVIITYMLTFFGLPELDROGRPKMFYQRIHDKC-- 235
QY 125 YRRPCH-----GEKGTGKGYCLERLYRVSL-----ACVCVR 156
DQ 236 YRRP-HFDAGQFVEHWDDEGARKGYC-----LYKVGCKGPTSYNACSTVR 279

Search completed: May 12, 2003, 01:59:40
Job time : 22 secs
```

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 12, 2003, 01:55:24 ; Search time 45 Seconds  
(without alignments)  
737.191 Million cell updates/sec

Title: US-10-037-591A-2  
Perfect score: 910  
Sequence: 1 MYQVAFVFLAMVGMGTHTYSHW.....ERRLYRYSVSLACVCRPRVMG 161

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organellae.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID  | Description         |
|------------|-------|-------------|--------|--------|---------------------|
| 1          | 904   | 99.3        | 161    | Q8WXB0 | Q8WXB0 homo sapien  |
| 2          | 709   | 77.9        | 169    | Q8VHH8 | Q8VHH8 mus musculus |
| 3          | 652   | 71.6        | 153    | Q8VHC9 | Q8VHC9 mus musculus |
| 4          | 126.5 | 13.9        | 202    | Q8TAD2 | Q8TAD2 homo sapien  |
| 5          | 114   | 12.5        | 111    | Q9BQI7 | Q9BQI7 rattus norv  |
| 6          | 107   | 11.8        | 162    | Q44146 | Q44146 caenorhabdi  |
| 7          | 95    | 10.4        | 141    | Q95156 | Q95156 bos taurus   |
| 8          | 87    | 9.6         | 499    | Q9GZ34 | Q9GZ34 trypanosoma  |
| 9          | 83    | 9.1         | 405    | Q9BU21 | Q9BU21 homo sapien  |
| 10         | 81    | 8.9         | 1394   | Q9VS89 | Q9VS89 drosophila   |
| 11         | 80.5  | 8.8         | 379    | Q9MKZ8 | Q9MKZ8 eptaretus    |
| 12         | 78.5  | 8.6         | 174    | Q8RVH7 | Q8RVH7 populus tre  |
| 13         | 78.5  | 8.6         | 206    | Q22687 | Q22687 caenorhabdi  |
| 14         | 78    | 8.6         | 459    | Q9DC55 | Q9DC55 mus musculus |
| 15         | 78    | 8.6         | 459    | Q9D624 | Q9D624 mus musculus |
| 16         | 78    | 8.6         | 459    | Q9CXA8 | Q9CXA8 mus musculus |

|    |      |     |      |    |        |                    |
|----|------|-----|------|----|--------|--------------------|
| 17 | 78   | 8.6 | 1090 | 10 | Q8S1E5 | Q8S1E5 oryza sativ |
| 18 | 76.5 | 8.4 | 1615 | 11 | Q9JIR4 | Q9JIR4 rattus norv |
| 19 | 76   | 8.4 | 2434 | 10 | Q94JB3 | Q94JB3 oryza sativ |
| 20 | 75.5 | 8.3 | 272  | 12 | Q36279 | Q36279 venezuelan  |
| 21 | 75.5 | 8.3 | 272  | 12 | Q36281 | Q36281 venezuelan  |
| 22 | 75.5 | 8.3 | 289  | 12 | Q9QAT3 | Q9QAT3 venezuelan  |
| 23 | 75.5 | 8.3 | 289  | 12 | Q9QAT2 | Q9QAT2 venezuelan  |
| 24 | 75.5 | 8.3 | 289  | 12 | Q9QAT1 | Q9QAT1 venezuelan  |
| 25 | 75.5 | 8.3 | 289  | 12 | Q9QAT0 | Q9QAT0 venezuelan  |
| 26 | 75.5 | 8.3 | 289  | 12 | Q9QAS9 | Q9QAS9 venezuelan  |
| 27 | 75.5 | 8.3 | 289  | 12 | Q9QAS8 | Q9QAS8 venezuelan  |
| 28 | 75.5 | 8.3 | 289  | 12 | Q9QAS7 | Q9QAS7 venezuelan  |
| 29 | 75.5 | 8.3 | 289  | 12 | Q9QAS6 | Q9QAS6 venezuelan  |
| 30 | 75.5 | 8.3 | 289  | 12 | Q9QAS5 | Q9QAS5 venezuelan  |
| 31 | 75.5 | 8.3 | 289  | 12 | Q9QAS4 | Q9QAS4 venezuelan  |
| 32 | 75.5 | 8.3 | 289  | 12 | Q9YJBI | Q9YJBI venezuelan  |
| 33 | 75.5 | 8.3 | 289  | 12 | Q9W9J3 | Q9W9J3 venezuelan  |
| 34 | 75.5 | 8.3 | 334  | 5  | Q961F6 | Q961F6 drosophila  |
| 35 | 75.5 | 8.3 | 369  | 5  | Q8SUP9 | Q8SUP9 encephalito |
| 36 | 75.5 | 8.3 | 432  | 4  | Q9NPM2 | Q9NPM2 homo sapien |
| 37 | 75.5 | 8.3 | 446  | 10 | Q9M0Y0 | Q9M0Y0 arabidopsis |
| 38 | 75.5 | 8.3 | 477  | 10 | Q94ON7 | Q94ON7 arabidopsis |
| 39 | 75.5 | 8.3 | 867  | 11 | Q9JLF9 | Q9JLF9 mus musculu |
| 40 | 75.5 | 8.3 | 874  | 5  | Q9VSE3 | Q9VSE3 drosophila  |
| 41 | 75.5 | 8.3 | 883  | 5  | Q8SX53 | Q8SX53 drosophila  |
| 42 | 75.5 | 8.3 | 898  | 4  | Q9UFZ4 | Q9UFZ4 homo sapien |
| 43 | 75.5 | 8.3 | 928  | 11 | Q9JLGO | Q9JLGO mus musculu |
| 44 | 75.5 | 8.3 | 1130 | 11 | Q9WUC2 | Q9WUC2 mus musculu |
| 45 | 75.5 | 8.3 | 1190 | 11 | Q9ES52 | Q9ES52 mus musculu |

ALIGNMENTS

RESULT 1

|        |                                                                                                                    |      |         |
|--------|--------------------------------------------------------------------------------------------------------------------|------|---------|
| Q8WXB0 | PRELIMINARY;                                                                                                       | PRT; | 161 AA. |
| ID     | Q8WXB0                                                                                                             |      |         |
| AC     | Q8WXB0;                                                                                                            |      |         |
| DT     | 01-MAR-2002 (TREMREL. 20, Created)                                                                                 |      |         |
| DT     | 01-MAR-2002 (TREMREL. 20, Last sequence update)                                                                    |      |         |
| DT     | 01-MAR-2002 (TREMREL. 20, Last annotation update)                                                                  |      |         |
| DE     | IL25.                                                                                                              |      |         |
| OS     | Homo sapiens (Human).                                                                                              |      |         |
| OC     | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;                                                            |      |         |
| OC     | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.                                                         |      |         |
| OX     | NCBI_TaxID=9606;                                                                                                   |      |         |
| RN     | [1]                                                                                                                |      |         |
| RP     | SEQUENCE FROM N.A.                                                                                                 |      |         |
| EX     | MEDLINE=21629216; PubMed=11754819;                                                                                 |      |         |
| RA     | Fort M.M., Cheung J., Yen D., Li J., Zurawski S.M., Lo S., Menon S.,                                               |      |         |
| RA     | Clifford T., Hunte B., Lesley R., Muchamuel T., Hurst S.D.,                                                        |      |         |
| RA     | Zurawski G., Leach M.W., Gorman D.M., Rennick D.M.;                                                                |      |         |
| RT     | "IL-25 Induces IL-4, IL-5, and IL-13 and Th2-Associated Pathologies In Vivo."                                      |      |         |
| RL     | Immunity 15:985-995(2001).                                                                                         |      |         |
| RN     | [2]                                                                                                                |      |         |
| RP     | SEQUENCE FROM N.A.                                                                                                 |      |         |
| RA     | Hurst S.D., Muchamuel T., Gorman D.M., Gilbert J.M., Clifford T.,                                                  |      |         |
| RA     | Kwan S., Menon S., Seymour B., Jackson C., Kung T., Brieland J.,                                                   |      |         |
| RA     | Zurawski S.M., Chapman R., Zurawski G., Coffman R.L.;                                                              |      |         |
| RT     | "New IL-17 family members promote Th1 or Th2 responses in the lung: In vivo function of the novel cytokine IL-25." |      |         |
| RL     | Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.                                                            |      |         |
| DR     | EMBL; AF458059; AAL57622.1;                                                                                        |      |         |
| SQ     | SEQUENCE 161 AA; 18537 MW; 32C85913FCFE151D CRC64;                                                                 |      |         |

Query Match 99.3%; Score 904; DB 4; Length 161;  
Best Local Similarity 100.0%; Pred. No. 1.le-89;  
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |   |                                                              |
|----|---|--------------------------------------------------------------|
| Qy | 1 | MYQVAFVFLAMVGMGTHTYSHWPCPSKGDTSSELLRWSTVPVPPLEPAPRHPHPSCA 60 |
| Db | 1 | MYQVAFVFLAMVGMGTHTYSHWPCPSKGDTSSELLRWSTVPVPPLEPAPRHPHPSCA 60 |

```
Qy 61 SEDGPLNSRAISPRYELDRDLNRLPDQLYHARCLPHCVSLQTGSHMDPRGNSSELLVHN 120
|||||
Db 61 SEDGPLNSRAISPRYELDRDLNRLPDQLYHARCLPHCVSLQTGSHMDPRGNSSELLVHN 120
|||||
Qy 121 QTVFYRRPCHGCKGTHGKCYCLRLRYRSLACVCRPRVM 160
|||||
Db 121 QTVFYRRPCHGCKGTHGKCYCLRLRYRSLACVCRPRVM 160
|||||

RESULT 2
Q8VHH8
ID Q8VHH8 PRELIMINARY; PRT; 169 AA.
AC Q8VHH8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE IL25.
GN IL17E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; PubMed=11754819;
RX Fort M.M., Cheung J., Yen D., Li J., Zurawski S.M., Lo S., Menon S.,
RA Clifford T., Hunte B., Lesley R., Muchamuel T., Kung T., Brieland J.,
RA Zurawski G., Leach M.W., Gorman D.M., Rennick D.M.;
RT "IL-25 Induces IL-4, IL-5, and IL-13 and Th2-Associated Pathologies In
RT Vivo.";
RL Immunity 15:985-995(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX Hurn S.D., Muchamuel T., Gorman D.M., Gilbert J.M., Clifford T.,
RA Kvan S., Menon S., Seymour B., Jackson C., Kung T., Brieland J.,
RA Zurawski S.M., Chapman R., Zurawski G., Coffman R.L.;
RT "New IL-17 family members promote Th1 or Th2 responses in the lung: In
RT vivo function of the novel cytokine IL-25.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF458060; AAL57623.1;
DR MGD; MGI:2155888; IL17e.
SQ SEQUENCE 169 AA; 19210 MW; CFAD2CEDE452C94D CRC64;

Query Match 77.9%; Score 709; DB 11; Length 169;
Best Local Similarity 76.8%; Pred. No. 1.2e-68;
Matches 129; Conservative 9; Mismatches 22; Indels 8; Gaps 1;

Qy 1 MYQVAFIAMVGTHTYSLRTOECSHLPSCPSKEQEPPEWLKWSASVSPPELSHT 52
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Db 1 MYQVAFIAMVGTHTYSLRTOECSHLPSCPSKEQEPPEWLKWSASVSPPELSHT 60
|||

Qy 53 RHPSCRASEDGPLNSRAISPRYELDRDLNRLPDQLYHARCLPHCVSLQTGSHMDPRG 112
|||||
Db 61 HHAESCRASKDGPLNSRAISPRYELDRDLNRLPDQLYHARCLPHCVSLQTGSHMDPLG 120
|||||

Qy 113 NSSELLYHNQTVFYRRPCHGCKGTHGKCYCLRLRYRSLACVCRPRVM 160
|||||
Db 121 NSVPLYHNQTVFYRRPCHGCKGTHGKCYCLRLRYRSLACVCRPRVM 168
|||||

RESULT 3
Q8VHC9
ID Q8VHC9 PRELIMINARY; PRT; 153 AA.
AC Q8VHC9;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Interleukin 17E (Fragment).
GN IL17E.
OS Mus musculus (Mouse).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21571724; PubMed=11714825;
RA Pan G., French D., Mao W., Maruoka M., Risser P., Lee J., Foster J.,
RA Aggarwal S., Nicholes K., Guillet S., Schow P., Gurney A.B.;
RT "Forced Expression of Murine IL-17E Induces Growth Retardation,
RT Jaundice, a Th2-Biased Response, and Multiorgan Inflammation in
RT Mice.";
RL J. Immunol. 167:6559-6567(2001).
DR EMBL; AY034088; AAK59816.1;
DR MGD; MGI:2155888; IL17e.
FT NON_TER 1
SQ SEQUENCE 153 AA; 17456 MW; A0BE897842E6EB39 CRC64;

Query Match 71.6%; Score 652; DB 11; Length 153;
Best Local Similarity 81.1%; Pred. No. 1.5e-62;
Matches 116; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Qy 18 SHWPCSPCKSGQDTSEELLRWSTVPVPPLEPARPNRHPESCRASEDGPLNSRAISPRY 77
|||||
Db 10 SHLPSCPSCKEQEPPEWLKWSASVSPPELSHTHHAESCRASKDGPLNSRAISPR 69
|||||

Qy 78 LDRLNRLPDQLYHARCLPHCVSLQTGSHMDPRGNSSELLYHNQTVFYRRPCHGCKGTHK 137
|||||
Db 70 LDRLNRLPDQLYHARCLPHCVSLQTGSHMDPLGNSVPLVHNQTVFYRRPCHGCKGTHR 129
|||||

Qy 138 GYCLRLRYRSLACVCRPRVM 160
|||||
Db 130 HYCLRLRYRSLACVCRPRVM 152
|||||

RESULT 4
Q8TAD2
ID Q8TAD2 PRELIMINARY; PRT; 202 AA.
AC Q8TAD2;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Interleukin 27 precursor (IL17D precursor).
GN IL27.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ENTIRE BRAIN;
RA Hadj-Slimane R., Bobe P.;
RT "Interleukin 27 (IL27): a newly identified cytokine.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hromas R.A., Starnes T.T.;
RT "IL-17D, A Novel Member of the IL-17 Family, Stimulates Cytokine
RT Production and Inhibits Hematopoiesis.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY078238; AAL86911.1;
DR EMBL; AF479775; AAM12734.1;
FT SIGNAL.
FT SIGNAL 1
SQ SEQUENCE 202 AA; 21893 MW; D171C5FB2DD039C3 CRC64;

Query Match 13.9%; Score 126.5; DB 4; Length 202;
Best Local Similarity 27.0%; Pred. No. 9e-06;
Matches 44; Conservative 17; Mismatches 69; Indels 33; Gaps 6;

Qy 20 WPCSPCKSGQ-----DTSEELLR-----WSTVPVPPLEPARPNRHP 56
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Db 14 WAAGAPRAGRPARPRGCAADRPPELLEQLYGLAAGVLSAFHHTLQLGPREQARNASCPA 73
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Q9DC55
ID Q9DC55 PRELIMINARY; PRT: 459 AA.
AC Q9DC55;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 1200003C23RIK protein.
GN 1200003C23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LUNG;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Staubli F., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Schriml L.M., Staubli F., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,
RA Brownstein M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK014681; BAB29502.1; -.
DR HSSP; P00743; ICCF.
DR MGD; MGI:1914114; 1200003C23RIK.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00001; EGF-like; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00041; C-TYPE_LECTIN_2; 1.
DR PROSITE; PS01186; EGF_2; 1.
SQ SEQUENCE 459 AA; 49065 MW; 6CB25D048A456A7B CRC64;

Query Match 8.6%; Score 78; DB 11; Length 459;
Best Local Similarity 25.4%; Pred. No. 3.8;
Matches 34; Conservative 12; Mismatches 44; Indels 44; Gaps 7;

QY 32 SEELLRWSTVP-----VPPLEPARPNR--HPESCRASEDGPLNSRAISPRWYELDRDLN 83
DB 87 SKDLFFWALERSISQCTQKEPLRGFSWLHPDS-EDSEDSPL-----PWVEEPQRS-- 137
QY 84 RLPQDLYHARCLPHCVSLQGTGSHMDPRGNSSELYHNQTVFYRRPCHEKGTGKCYCLER 143
DB 138 -----CTVRKCAALQATRGVEPAGWKEMRCHLRT-----DGYLCK- 172
QY 144 RLYRVSLACVCVRP 157
DB 173 --YQFEVLCPPAPRP 184

Search completed: May 12, 2003, 02:00:42
Job time : 47 secs

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GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: May 12, 2003, 01:59:09 ; Search time 23 Seconds  
(without alignments)  
205.960 Million cell updates/sec

Title: US-10-037-591A-2

Perfect score: 910

Sequence: 1 MYQVAPLANMGHTTYSHW.....ERRLYRSLACVCPVRVMG 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 121   | 13.3        | 205    | 4     | US-09-724-864-37  |
| 2          | 120.5 | 13.2        | 153    | 1     | US-08-514-014-12  |
| 3          | 120.5 | 13.2        | 153    | 2     | US-08-833-823-12  |
| 4          | 120.5 | 13.2        | 163    | 3     | US-09-034-810-2   |
| 5          | 120.5 | 13.2        | 163    | 3     | US-08-685-239-2   |
| 6          | 96.5  | 10.6        | 155    | 4     | US-08-432-994A-8  |
| 7          | 92.5  | 10.2        | 151    | 2     | US-08-620-694A-8  |
| 8          | 92.5  | 10.2        | 151    | 3     | US-09-034-810-6   |
| 9          | 92.5  | 10.2        | 151    | 3     | US-09-022-255-8   |
| 10         | 92.5  | 10.2        | 151    | 3     | US-09-022-696-8   |
| 11         | 92.5  | 10.2        | 151    | 3     | US-08-685-239-6   |
| 12         | 92.5  | 10.2        | 151    | 3     | US-09-022-253-8   |
| 13         | 92.5  | 10.2        | 151    | 3     | US-09-022-260-8   |
| 14         | 92.5  | 10.2        | 151    | 4     | US-09-022-259-8   |
| 15         | 92.5  | 10.2        | 151    | 4     | US-09-022-257-8   |
| 16         | 92.5  | 10.2        | 151    | 4     | US-08-432-994A-4  |
| 17         | 91    | 10.0        | 150    | 3     | US-09-034-810-4   |
| 18         | 91    | 10.0        | 150    | 3     | US-08-685-239-4   |
| 19         | 91    | 10.0        | 150    | 4     | US-08-432-994A-2  |
| 20         | 86    | 9.5         | 158    | 2     | US-08-620-694A-7  |
| 21         | 86    | 9.5         | 158    | 3     | US-09-022-255-7   |
| 22         | 86    | 9.5         | 158    | 3     | US-09-022-696-7   |
| 23         | 86    | 9.5         | 158    | 3     | US-09-022-253-7   |
| 24         | 86    | 9.5         | 158    | 3     | US-09-022-260-7   |
| 25         | 86    | 9.5         | 158    | 4     | US-09-022-259-7   |
| 26         | 86    | 9.5         | 158    | 4     | US-09-022-257-7   |
| 27         | 86    | 9.5         | 158    | 4     | US-08-432-994A-10 |

28 76.5 8.4 1323 1 US-08-026-138E-4 Sequence 4, Appli  
29 75.5 8.3 1185 4 US-08-664-962B-2 Sequence 2, Appli  
30 75.5 8.3 1185 4 US-09-311-743-2 Sequence 2, Appli  
31 74.5 8.2 514 4 US-08-974-549A-605 Sequence 605, App  
32 74.5 8.2 807 4 US-08-974-549A-5 Sequence 5, Appli  
33 74.5 8.2 1132 3 US-08-851-843A-225 Sequence 225, App  
34 74.5 8.2 1132 4 US-08-974-549A-2 Sequence 2, Appli  
35 74.5 8.2 1132 4 US-08-974-549A-344 Sequence 344, App  
36 74.5 8.2 1132 4 US-08-854-050-225 Sequence 225, App  
37 74.5 8.2 1132 4 US-09-430-323-225 Sequence 225, App  
38 74.5 8.2 1132 4 US-09-128-354-2 Sequence 2, Appli  
39 74.5 8.2 1132 4 US-09-675-321-2 Sequence 2, Appli  
40 74.5 8.2 1132 4 US-09-052-919-2 Sequence 2, Appli  
41 74.5 8.2 1154 4 US-08-974-549A-611 Sequence 611, App  
42 74.5 8.2 1189 4 US-08-974-549A-613 Sequence 613, App  
43 74.5 8.2 1200 4 US-08-974-549A-612 Sequence 612, App  
44 74.5 8.2 1285 4 US-08-974-549A-600 Sequence 600, App  
45 74.5 8.2 1407 4 US-08-974-549A-628 Sequence 628, App

#### ALIGNMENTS

##### RESULT 1

US-09-724-864-37  
; Sequence 37, Application US/09724864

; Patent No. 6380362

; GENERAL INFORMATION:

...; APPLICANT: Watson, James D

; APPLICANT: Murison, James G.

; TITLE OF INVENTION: Polynucleotides, polypeptides expressed

; TITLE OF INVENTION: by the polynucleotides and methods for their use.

; FILE REFERENCE: 11000.1050U1

; CURRENT APPLICATION NUMBER: US/09/724,864

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678

; PRIOR FILING DATE: 1999-12-23

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 37

; LENGTH: 205

; TYPE: PRT

; ORGANISM: Mouse

US-09-724-864-37

Query Match 13.3%; Score 121; DB 4; Length 205;

Best Local Similarity 27.1%; Pred. No. 1.2e-05;

Matches 42; Conservative 19; Mismatches 58; Indels 36; Gaps 7;

QY 25 PSKGQDTSELLR-----WSTVPVPPLEPAPRPNRHPSCRASE---DGPLN 67

DB 35 PRDCADRPPELLEQLYGRLAAGVLSAFHHTLQLGPREQARNASCAGGAADRFRPPTN 94

QY 68 SRAISPWRYELDRDLNRLPDQLYHARCLPHCVSLGTGSHMDPRGNSSELYHNOTVF--- 124

DB 95 LRSVSPWYARISYDPAFPYLPYAVCLRGCL---TGLY----GEEDFRFRSTPVSFA 147

QY 125 --YRR--PCHGEKGTGKGYCLRLRLRYRSLACVCV 155

DB 148 VVLRRTAACAGGRSVYAEHVI-----TIPVGCTCV 177

##### RESULT 2

US-08-514-014-12

; Sequence 12, Application US/08514014

; Patent No. 5707829

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; APPLICANT: McCoy, John

; APPLICANT: Kelleher, Kerry

; APPLICANT: Carlin, McKough

; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS

; TITLE OF INVENTION: ENCODED THEREBY

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Query Match      13.2%; Score 120.5; DB 2; Length 153;
Best Local Similarity 26.3%; Pred. No. 9.3e-06;
Matches 40; Conservative 22; Mismatches 49; Indels 41; Gaps 7;

QY 15 HTYSHWSPSCPSKQDSELLRWSTVPV-----PLEPARPNRHPECSRASEDPLNSRA 70
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 28 HTFPQKDESCP-----PVPGSGMKLDGIIN-----ENORVSMRNIESRS 68

QY 71 ISPWRYELDRDLNRLPODLYHARCLCPHCYSVLOTGSGHMDPRGNSLEYLHN---QTVFY 125

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| Db | 69  | TSPANTVTWDPNRYSEVVQAOCRNLGCI | NAQ-----GKEDI       | SMNSVP  | IQQETLVV | 120 |
| Qy | 126 | RRPCHGEKGT                   | HKGYCYCLERRLLRY     | SVSLACV | CVVR     | 157 |
| Db | 121 | RRK---HGG                    | SVSFOLEKVL--VTVGTCV | TP      |          | 147 |

RESULT 4  
US-09-034-810-2  
; Sequence 2, Application US/09034810  
; Patent No. 6043344

APPLICANT: MI, Sha  
 APPLICANT: Neben, Steven  
 APPLICANT: Giannotti, JoAnn  
 APPLICANT: Golden/Fleet, Margaret  
 TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genetics Institute, Inc.  
 STREET: 87 CambridgePark Drive  
 CITY: Cambridge  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02140  
 COMPUTER READABLE FORM: disk  
 MEDIUM TYPE: Floppy  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/034,810  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/685,239

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-685-239-2

Query Match 13.2%; Score 120.5; DB 3; Length 163;
Best Local Similarity 26.3%; Pred. No. 1e-05;
Matches 40; Conservative 22; Mismatches 49; Indels 41; Gaps 7;

QY 15 HTYSHWSPCCPSKGDITSELLRWSTVPV-----PLEPARENRRHPESCRASEDGPLNSRA 70
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DB 38 HTFFQKPESCP-----PVPGGSKMLDIGIIN---ENQRVSMRSNIESRS 78

QY 71 ISPWRYELDRDLNRLPODLYHARCLCPHCYSLOTGSHMDPRGNSSELYHN-----QTVFY 125
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 79 TSPWNYYTWDPNRPYSEVVQAOQRNLGCINAQ-----GKEDISWNSVPIQOETLVV 130

QY 126 RRPCGEGKHGKCYCLERRLYRVSACVCYRP 157
   || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 131 RKR---HGGCSVSFQLEKVL--VTVGCTCVTP 157

RESULT 6
US-08-432-994A-8
; Sequence 8, Application US/08432994A
; Patent No. 6274711
; GENERAL INFORMATION:
; APPLICANT: Goustein, Pierre
; APPLICANT: Bouvier, Eric

```

APPLICANT: Lebecque, Serge J.E.  
 APPLICANT: Djossou, Odile  
 APPLICANT: Banchereau, Jacques  
 TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND  
 TITLE OF INVENTION: RELATED REAGENTS  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DNAX Research Institute  
 STREET: 901 California Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/432,994A  
 FILING DATE: 02-MAY-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/250,846  
 FILING DATE: 27-MAY-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/177,747  
 FILING DATE: 05-JAN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/077,203  
 FILING DATE: 14-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ching, Edwin P.  
 REGISTRATION NUMBER: 34,090  
 REFERENCE/DOCKET NUMBER: DX0388K3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-852-9196  
 TELEFAX: 415-496-1200  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 155 amino acids

; ORIGINAL SOURCE:

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Db   51 NWTSTSKRASD---YYNRSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCYNAD-----99

Qy   112 GNSellyHNOTVFYRRPC----HGEGKTHKGycLERRLRYRVSLACVcVRPRV 159
      || : || :|| :| :| :|| : | :| :|| :|| :|| :|
Db   100 GNVD--YHMNSVPtIQOEILvRKGHGCPcNSFRLEKML--VTVGCTCVTPIV 147
      || : || :|| :| :| :|| : | :| :|| :|| :|| :|

RESULT 9
US-09-022-255-8
; Sequence 8, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: NO. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpesvirus Saimiri
; STRAIN: ORf13
; US-09-022-255-8

Query Match          10.2%; Score 92.5; DB 3; Length 151;
Best Local Similarity 27.7%; Pred. No. 0.011;
Matches    31; Conservative    19; Mismatches    43; Indels    19; Gaps

Qy   52 NRIPESCRASDEGPLNSRATSPWRYEldRDNLRLPDQLYHARCtPHCvSLOtGSMDPR 111
      | : | ||| :|| :||| :| :| :|| :| :| :|| :|
Db   51 NWNTSSKRASD---YYNRSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCYNAD-----99
      | : | ||| :|| :||| :| :| :|| :| :| :|| :|

Qy   112 GNSellyHNOTVFYRRPC----HGEGKTHKGycLERRLRYRVSLACVcVRPRV 159
      || : || :|| :| :| :|| : | :| :|| :|| :|| :|
Db   100 GNVD--YHMNSVPtIQOEILvRKGHGCPcNSFRLEKML--VTVGCTCVTPIV 147
      || : || :|| :| :| :|| : | :| :|| :|| :|| :|
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpesvirus Salmiri
; STRAIN: ORE13
; US-09-022-257-8

Query Match 10.2%; Score 92.5; DB 4; Length 151;
Best Local Similarity 27.7%; Pred. No. 0.011;
Matches 31; Conservative 19; Mismatches 43; Indels 19; Gaps 5;

QY 52 NRHPESCRASEDGPLNSRAISPRYELDRNLRLPQDLYHARCLCPHCYSLQGTGSHMDPR 111
| : | ||| : : || : : || : : || :
DB 51 NWTSSKRASD--YYNRSTSPWTLHRNEDQDRYPSVWEAKCRYLGCVNAD----- 99
| : | ||| : : || : : || : : || :

QY 112 GNSellyHMQTVFYRRPC----HGEKGTHTKGYCLERRLYRVSLACVCRPRV 159
| : | || : || : : | : : | : : | :
DB 100 GNVQ--YHMNSVPIQOEILVVRKGHPCPNSFLEKML--VTVGCTCTVPIV 147
| : | || : || : : | : : | : : | :

Search completed: May 12, 2003, 02:02:52
Job time : 24 secs
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GenCore version 5.1.4\_p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 12, 2003, 01:58:09 ; Search time 29 Seconds  
(without alignments)  
510.901 Million cell updates/sec

Title: US-10-037-591A-2

Perfect score: 910

Sequence: 1 MYQVAFVFLAMVGMTHYSHW.....ERRLYRVSLACVCRPRVMG 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description       |
|------------|-------|---------------|--------|-------|-------------------|
| 1          | 910   | 100.0         | 161    | 10    | US-09-886-404-2   |
| 2          | 898   | 98.7          | 177    | 9     | US-09-874-503-6   |
| 3          | 898   | 98.7          | 177    | 9     | US-10-000-157-6   |
| 4          | 898   | 98.7          | 177    | 9     | US-10-063-547-156 |
| 5          | 898   | 98.7          | 177    | 9     | US-09-816-744-6   |
| 6          | 898   | 98.7          | 177    | 9     | US-09-747-259-6   |
| 7          | 898   | 98.7          | 177    | 9     | US-10-063-616-156 |
| 8          | 898   | 98.7          | 177    | 9     | US-10-063-502-156 |
| 9          | 898   | 98.7          | 177    | 9     | US-10-063-518-156 |
| 10         | 898   | 98.7          | 177    | 9     | US-10-063-598-156 |
| 11         | 898   | 98.7          | 177    | 9     | US-10-227-693-156 |
| 12         | 898   | 98.7          | 177    | 9     | US-09-908-827-6   |
| 13         | 898   | 98.7          | 177    | 9     | US-10-213-181-18  |
| 14         | 898   | 98.7          | 177    | 9     | US-10-063-567-156 |
| 15         | 898   | 98.7          | 177    | 9     | US-10-063-538-156 |
| 16         | 898   | 98.7          | 177    | 9     | US-10-063-599-156 |
| 17         | 898   | 98.7          | 177    | 9     | US-10-212-912-18  |
| 18         | 898   | 98.7          | 177    | 9     | US-10-213-044-18  |
| 19         | 898   | 98.7          | 177    | 9     | US-10-063-595-156 |

|    |       |      |     |    |                   |                   |
|----|-------|------|-----|----|-------------------|-------------------|
| 20 | 898   | 98.7 | 177 | 12 | US-10-006-867-156 | Sequence 156, App |
| 21 | 709   | 77.9 | 169 | 10 | US-09-886-404-4   | Sequence 4, Appli |
| 22 | 670   | 73.6 | 159 | 10 | US-09-886-404-10  | Sequence 10, Appl |
| 23 | 170.5 | 18.7 | 206 | 10 | US-09-854-280-24  | Sequence 24, Appl |
| 24 | 170.5 | 18.7 | 206 | 10 | US-09-854-208-24  | Sequence 24, Appl |
| 25 | 165.5 | 18.2 | 197 | 9  | US-09-874-503-4   | Sequence 4, Appli |
| 26 | 165.5 | 18.2 | 197 | 9  | US-10-000-157-4   | Sequence 4, Appli |
| 27 | 165.5 | 18.2 | 197 | 9  | US-10-036-041-11  | Sequence 11, Appl |
| 28 | 165.5 | 18.2 | 197 | 9  | US-09-320-713-29  | Sequence 29, Appl |
| 29 | 165.5 | 18.2 | 197 | 9  | US-09-816-744-4   | Sequence 4, Appli |
| 30 | 165.5 | 18.2 | 197 | 9  | US-09-747-259-4   | Sequence 4, Appli |
| 31 | 165.5 | 18.2 | 197 | 9  | US-10-035-855-11  | Sequence 11, Appl |
| 32 | 165.5 | 18.2 | 197 | 9  | US-10-174-590-448 | Sequence 448, App |
| 33 | 165.5 | 18.2 | 197 | 9  | US-10-176-758-448 | Sequence 448, App |
| 34 | 165.5 | 18.2 | 197 | 9  | US-10-175-737-448 | Sequence 448, App |
| 35 | 165.5 | 18.2 | 197 | 9  | US-10-173-706-448 | Sequence 448, App |
| 36 | 165.5 | 18.2 | 197 | 9  | US-10-175-738-448 | Sequence 448, App |
| 37 | 165.5 | 18.2 | 197 | 9  | US-10-175-752-448 | Sequence 448, App |
| 38 | 165.5 | 18.2 | 197 | 9  | US-10-176-482-448 | Sequence 448, App |
| 39 | 165.5 | 18.2 | 197 | 9  | US-10-176-757-448 | Sequence 448, App |
| 40 | 165.5 | 18.2 | 197 | 9  | US-10-176-913-448 | Sequence 448, App |
| 41 | 165.5 | 18.2 | 197 | 9  | US-10-180-552-448 | Sequence 448, App |
| 42 | 165.5 | 18.2 | 197 | 9  | US-10-180-557-448 | Sequence 448, App |
| 43 | 165.5 | 18.2 | 197 | 9  | US-09-931-836-11  | Sequence 11, Appl |
| 44 | 165.5 | 18.2 | 197 | 9  | US-10-173-700-448 | Sequence 448, App |
| 45 | 165.5 | 18.2 | 197 | 9  | US-10-174-572-448 | Sequence 448, App |

#### ALIGNMENTS

RESULT 1  
US-09-886-404-2  
; Sequence 2, Application US/09886404  
; Patent No. US20020037524A1  
; GENERAL INFORMATION:  
; APPLICANT: Medlock, Eugene  
; APPLICANT: Yeh, Richard  
; APPLICANT: Silbiger, Scott M.  
; APPLICANT: Elliot, Gary S.  
; APPLICANT: Nguyen, Hung O.  
; APPLICANT: Jing, Shugian  
; TITLE OF INVENTION: IU-17 Like Molecules and Uses Thereof  
; FILE REFERENCE: 01017/37128B  
; CURRENT APPLICATION NUMBER: US/09/886,404  
; CURRENT FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 09/810,384  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/266,159  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 60/213,125  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-886-404-2

Query Match 100.0%; Score 910; DB 10; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.5e-78;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYQVAFVFLAMVGMTHYSHWPSCCPKSGDITSEELLRWSTVPVPLEPARNRHPESCRA 60  
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Db 1 MYQVAFVFLAMVGMTHYSHWPSCCPKSGDITSEELLRWSTVPVPLEPARNRHPESCRA 60

Qy 61 SEDGFLNSRAISPRYELDRDLNRLPQDLYHARCLCPHCVSLSQTGSHMDPRGNSELYNHN 120  
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Db 61 SEDGFLNSRAISPRYELDRDLNRLPQDLYHARCLCPHCVSLSQTGSHMDPRGNSELYNHN 120

Qy 121 QTVFYRRPCHGEKTHKCYCLERRLYRSLACVCRPRVMG 161

Db 121 QTFFRRPCHGEKTHKGYCLERRLYRSLACVCRPRVMG 161  
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RESULT 2  
US-09-874-503-6  
; Sequence 6, Application US/09874503  
; Patent No. US2002017188A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jian  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Li, Hanzhong  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Hymowitz, Sarah G.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Starovasanik, Melissa A.  
; APPLICANT: VanLookeren, Menno  
; APPLICANT: Vandlen, Richard  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Yansura, Daniel  
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
; CURRENT APPLICATION NUMBER: US/09/874,503  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/253,646  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 60/244,072  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/242,837  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/175,481  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: US 60/191,007  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/213,807  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: US 60/172,096  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: US 60/138,387  
; PRIOR FILING DATE: 1999-06-09  
; PRIOR APPLICATION NUMBER: US 60/134,287  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: US 60/131,022  
; PRIOR FILING DATE: 1999-04-26  
; PRIOR APPLICATION NUMBER: US 60/130,232  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: US 60/113,621  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: US 60/085,579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: US 09/854,208  
; PRIOR FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: US 09/854,280  
; PRIOR FILING DATE: 2001-05-20  
; PRIOR APPLICATION NUMBER: US 09/816,744  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: US 09/747,259  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: US 09/644,848  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: US 09/380,142  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: US 09/380,138  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: US 09/311,832  
; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: US PCT/US01/06520  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: US PCT/US00/34956  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: US PCT/US00/32678  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US PCT/US00/30873  
; PRIOR FILING DATE: 2000-11-10  
; PRIOR APPLICATION NUMBER: US PCT/US00/23328  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US PCT/US00/15264  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: US PCT/US00/07532  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US PCT/US00/05841  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: US PCT/US00/05601  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US PCT/US00/04341  
; PRIOR FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: US PCT/US99/31274  
; PRIOR FILING DATE: 1999-12-30  
; PRIOR APPLICATION NUMBER: US PCT/US99/10733  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: US PCT/US99/05028  
; PRIOR FILING DATE: 1999-03-08  
; NUMBER OF SEQ ID NOS: 39  
; SEQ ID NO 6  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-874-503-6  
Query Match 98.7%; Score 898; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.8e-77;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 QVAFALAMVMTHTYSHWPCSCPSKGQDTSEELLRWSTVPPPLEPARNRHPESCRASE 62  
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Db 19 QVAFALAMVMTHTYSHWPCSCPSKGQDTSEELLRWSTVPPPLEPARNRHPESCRASE 78  
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QY 63 DGPLNSRAISPRWYELDRDLNRLPQDLYHARCLPHCVSLQTSGLSHMDPRGNSSELYHNQT 122  
|||||  
Db 79 DGPLNSRAISPRWYELDRDLNRLPQDLYHARCLPHCVSLQTSGLSHMDPRGNSSELYHNQT 138  
|||||  
QY 123 VFYRRPCHGEKTHKGYCLERRLYRSLACVCRPRVMG 161  
|||||  
Db 139 VFYRRPCHGEKTHKGYCLERRLYRSLACVCRPRVMG 177  
|||||  
RESULT 3  
US-10-000-157-6  
; Sequence 6, Application US/100000157  
; Publication No. US20020182673A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jian  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul L.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Li, Hanzhong  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Hymowitz, Sarah  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Starovasanik, Melissa.  
; APPLICANT: VanLookeren, Menno  
; APPLICANT: Vandlen, Richard  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William  
; APPLICANT: Yansura, Daniel

;; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

;; FILE REFERENCE: P1381R1C1P4(US)  
;; CURRENT APPLICATION NUMBER: US/10/000,157

;; CURRENT FILING DATE: 2001-10-30

;; PRIOR APPLICATION NUMBER: 60/085579

;; PRIOR FILING DATE: 1998-05-15

;; PRIOR APPLICATION NUMBER: 60/113621

;; PRIOR FILING DATE: 1998-12-23

;; PRIOR APPLICATION NUMBER: 60/130232

;; PRIOR FILING DATE: 1999-04-21

;; PRIOR APPLICATION NUMBER: 60/131022

;; PRIOR FILING DATE: 1999-04-26

;; PRIOR APPLICATION NUMBER: 60/134287

;; PRIOR FILING DATE: 1999-05-14

;; PRIOR APPLICATION NUMBER: 60/138387

;; PRIOR FILING DATE: 1999-06-09

;; PRIOR APPLICATION NUMBER: 60/172096

;; PRIOR FILING DATE: 1999-12-23

;; PRIOR APPLICATION NUMBER: 60/175481

;; PRIOR FILING DATE: 2000-01-11

;; PRIOR APPLICATION NUMBER: 60/191007

;; PRIOR FILING DATE: 2000-03-21

;; PRIOR APPLICATION NUMBER: 60/213807

;; PRIOR FILING DATE: 2000-06-22

;; PRIOR APPLICATION NUMBER: 60/242837

;; PRIOR FILING DATE: 2000-10-24

;; PRIOR APPLICATION NUMBER: 60/244072

;; PRIOR FILING DATE: 2000-10-26

;; PRIOR APPLICATION NUMBER: 60/253646

;; PRIOR FILING DATE: 2000-11-28

;; PRIOR APPLICATION NUMBER: 09/311832

;; PRIOR FILING DATE: 1999-05-14

;; PRIOR APPLICATION NUMBER: 09/380138

;; PRIOR FILING DATE: 1999-08-25

;; PRIOR APPLICATION NUMBER: 09/380142

;; PRIOR FILING DATE: 1999-08-25

;; PRIOR APPLICATION NUMBER: 09/644848

;; PRIOR FILING DATE: 2000-08-22

;; PRIOR APPLICATION NUMBER: 09/747259

;; PRIOR FILING DATE: 2000-12-20

;; PRIOR APPLICATION NUMBER: 09/816744

;; PRIOR FILING DATE: 2001-03-22

;; PRIOR APPLICATION NUMBER: 09/854208

;; PRIOR FILING DATE: 2001-05-10

;; PRIOR APPLICATION NUMBER: 09/854280

;; PRIOR FILING DATE: 2001-05-10

;; PRIOR APPLICATION NUMBER: 09/874503

;; PRIOR FILING DATE: 2001-06-05

;; PRIOR APPLICATION NUMBER: 09/908827

;; PRIOR FILING DATE: 2001-07-18

;; PRIOR APPLICATION NUMBER: 09/918585

;; PRIOR FILING DATE: 2001-07-30

;; PRIOR APPLICATION NUMBER: 09/929404

;; PRIOR FILING DATE: 2001-08-13

;; PRIOR APPLICATION NUMBER: 09/931836

;; PRIOR FILING DATE: 2001-08-16

;; PRIOR APPLICATION NUMBER: PCT/US99/05028

;; PRIOR FILING DATE: 1999-03-08

;; PRIOR APPLICATION NUMBER: PCT/US99/10733

;; PRIOR FILING DATE: 1999-05-14

;; PRIOR APPLICATION NUMBER: PCT/US99/31274

;; PRIOR FILING DATE: 1999-12-30

;; PRIOR APPLICATION NUMBER: PCT/US00/04341

;; PRIOR FILING DATE: 2000-02-18

;; PRIOR APPLICATION NUMBER: PCT/US00/05601

;; PRIOR FILING DATE: 2001-03-01

;; PRIOR APPLICATION NUMBER: PCT/US00/05841

;; PRIOR FILING DATE: 2000-03-02

;; PRIOR APPLICATION NUMBER: PCT/US00/07532

;; PRIOR FILING DATE: 2000-03-21

;; PRIOR APPLICATION NUMBER: PCT/US00/15264

;; PRIOR FILING DATE: 2000-06-02

;; PRIOR APPLICATION NUMBER: PCT/US00/23328

;; PRIOR FILING DATE: 2000-08-24

;; PRIOR APPLICATION NUMBER: PCT/US00/30873

;; PRIOR FILING DATE: 2000-11-10

;; PRIOR APPLICATION NUMBER: PCT/US00/32678

;; PRIOR FILING DATE: 2000-12-01

;; PRIOR APPLICATION NUMBER: PCT/US00/34956

;; PRIOR FILING DATE: 2000-12-20

;; PRIOR APPLICATION NUMBER: PCT/US01/06520

;; PRIOR FILING DATE: 2001-02-28

;; PRIOR APPLICATION NUMBER: PCT/US01/17800

;; PRIOR FILING DATE: 2001-06-01

;; PRIOR APPLICATION NUMBER: PCT/US01/19692

;; PRIOR FILING DATE: 2001-06-20

;; PRIOR APPLICATION NUMBER: PCT/US01/21066

;; PRIOR FILING DATE: 2001-06-29

;; PRIOR APPLICATION NUMBER: PCT/US01/21735

;; PRIOR FILING DATE: 2001-07-09

;; NUMBER OF SEQ ID NOS: 39

;; SEQ ID NO 6

;; LENGTH: 177

;; TYPE: PRT

;; ORGANISM: Homo Sapien

;; US-10-000-157-6

Query Match 98.7%; Score 898; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 3.8e-77;

Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QVAFAMVGMGTHYSHWPCSCPSKGDTSSELLRWSTVVPPLPARNRHPESCRASE 62

Db 19 QVAFAMVGMGTHYSHWPCSCPSKGDTSSELLRWSTVVPPLPARNRHPESCRASE 78

Qy 63 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLPCHVSLQTGSHMDPRGNSSELYHNQT 122

Db 79 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLPCHVSLQTGSHMDPRGNSSELYHNQT 138

Qy 123 VFYRPPCHGCKTHGKCYCLERLRVSLACVCRPRVMG 161

Db 139 VFYRPPCHGCKTHGKCYCLERLRVSLACVCRPRVMG 177

RESULT 4

US-10-063-547-156

;; Sequence 156, Application US/10063547

;; Publication No. US20020182638A1

;; GENERAL INFORMATION:

;; APPLICANT: Eaton, Dan L.

;; APPLICANT: Filvaroff, Ellen

;; APPLICANT: Gerritsen, Mary E.

;; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul J.

;; APPLICANT: Grimaldi, Christopher J.

;; APPLICANT: Gurney, Austin L.

;; APPLICANT: Watanabe, Colin K.

;; APPLICANT: Wood, William I.

;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

;; TITLE OF INVENTION: ACIDS ENCODING THE SAME

;; FILE REFERENCE: P3230R1C1

;; CURRENT APPLICATION NUMBER: US/10/063,547

;; CURRENT FILING DATE: 2002-05-02

;; Prior Application removed - See File Wrapper or Palm

;; NUMBER OF SEQ ID NOS: 170

;; SEQ ID NO 156

;; LENGTH: 177

;; TYPE: PRT

;; ORGANISM: Homo Sapien

;; US-10-063-547-156

Query Match 98.7%; Score 898; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 3.8e-77;

Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QVAFAMVGMGTHYSHWPCSCPSKGDTSSELLRWSTVVPPLPARNRHPESCRASE 62

```

Db 19 QVAFVAMVGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPLEPARPNRHPSCRASE 78
QY 63 DGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVCVSLQTSQSHMDPRGNSELYHNQT 122
Db 79 DGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVCVSLQTSQSHMDPRGNSELYHNQT 138
QY 123 VFYRRPCHGEKGTGKGYCLERRLYRVSLACVCRVRVMG 161
Db 139 VFYRRPCHGEKGTGKGYCLERRLYRVSLACVCRVRVMG 177

RESULT 5
US-09-816-744-6
; Sequence 6, Application US/09816744
; Publication No. US20030003546A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P2(US)
; CURRENT APPLICATION NUMBER: US/09/816,744
; PRIOR FILING DATE: 2001-03-22
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 6
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-816-744-6

Query Match 98.7%; Score 898; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.8e-77;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QVAFVAMVGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPLEPARPNRHPSCRASE 62
Db 19 QVAFVAMVGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPLEPARPNRHPSCRASE 78
QY 63 DGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVCVSLQTSQSHMDPRGNSELYHNQT 122
Db 79 DGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVCVSLQTSQSHMDPRGNSELYHNQT 138
QY 123 VFYRRPCHGEKGTGKGYCLERRLYRVSLACVCRVRVMG 161
Db 139 VFYRRPCHGEKGTGKGYCLERRLYRVSLACVCRVRVMG 177

RESULT 6
US-09-747-259-6
; Sequence 6, Application US/09747259
; Publication No. US20030008815A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul

```

```

; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 6
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-747-259-6

Query Match 98.7%; Score 898; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.8e-77;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QVAFVAMVGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPLEPARPNRHPSCRASE 62
Db 19 QVAFVAMVGTHTYSHWPCSCPKGQDTSEELLRWSTVPVPLEPARPNRHPSCRASE 78
QY 63 DGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVCVSLQTSQSHMDPRGNSELYHNQT 122
Db 79 DGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVCVSLQTSQSHMDPRGNSELYHNQT 138
QY 123 VFYRRPCHGEKGTGKGYCLERRLYRVSLACVCRVRVMG 161
Db 139 VFYRRPCHGEKGTGKGYCLERRLYRVSLACVCRVRVMG 177

RESULT 7
US-10-063-616-156

```

; Sequence 156, Application US/10063616  
; Publication No. US20030013855A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,616  
; CURRENT FILING DATE: 2002-05-03  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 156  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-063-616-156

Query Match 98.7%; Score 898; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.8e-77;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QVAFAMVMGTHYSHWPCSCPSKGQDTSEELLRWSTVPPPLEPARNRHPESCRASE 62  
Db 19 QVAFAMVMGTHYSHWPCSCPSKGQDTSEELLRWSTVPPPLEPARNRHPESCRASE 78  
Qy 63 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCHVCVSLQSGHMDPRGNSSELYHNQT 122  
Db 79 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCHVCVSLQSGHMDPRGNSSELYHNQT 138  
Qy 123 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 161  
Db 139 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 177  
Qy 123 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 161  
Db 139 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 177

RESULT 8  
US-10-063-502-156  
; Sequence 156, Application US/10063502  
; Publication No. US20030023042A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,502  
; CURRENT FILING DATE: 2002-05-01  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 156  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-063-502-156

Query Match 98.7%; Score 898; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.8e-77;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QVAFAMVMGTHYSHWPCSCPSKGQDTSEELLRWSTVPPPLEPARNRHPESCRASE 62  
Db 19 QVAFAMVMGTHYSHWPCSCPSKGQDTSEELLRWSTVPPPLEPARNRHPESCRASE 78  
Qy 63 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCHVCVSLQSGHMDPRGNSSELYHNQT 122  
Db 79 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCHVCVSLQSGHMDPRGNSSELYHNQT 138  
Qy 123 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 161  
Db 139 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 177

RESULT 9  
US-10-063-518-156  
; Sequence 156, Application US/10063518  
; Publication No. US20030049735A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,518  
; CURRENT FILING DATE: 2002-05-01  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 156  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-063-518-156

Query Match 98.7%; Score 898; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.8e-77;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QVAFAMVMGTHYSHWPCSCPSKGQDTSEELLRWSTVPPPLEPARNRHPESCRASE 62  
Db 19 QVAFAMVMGTHYSHWPCSCPSKGQDTSEELLRWSTVPPPLEPARNRHPESCRASE 78  
Qy 63 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCHVCVSLQSGHMDPRGNSSELYHNQT 122  
Db 79 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCHVCVSLQSGHMDPRGNSSELYHNQT 138  
Qy 123 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 161  
Db 139 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 177

RESULT 10  
US-10-063-598-156  
; Sequence 156, Application US/10063598  
; Publication No. US20030050462A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,598  
; CURRENT FILING DATE: 2002-05-01  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 156  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-063-598-156

Query Match 98.7%; Score 898; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.8e-77;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QVAFAMVMGTHYSHWPCSCPSKGQDTSEELLRWSTVPPPLEPARNRHPESCRASE 62  
Db 19 QVAFAMVMGTHYSHWPCSCPSKGQDTSEELLRWSTVPPPLEPARNRHPESCRASE 78  
Qy 63 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCHVCVSLQSGHMDPRGNSSELYHNQT 122  
Db 79 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCHVCVSLQSGHMDPRGNSSELYHNQT 138  
Qy 123 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 161  
Db 139 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 177

RESULT 9  
US-10-063-518-156  
; Sequence 156, Application US/10063518  
; Publication No. US20030049735A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,518  
; CURRENT FILING DATE: 2002-05-01  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 156  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-063-518-156

Query Match 98.7%; Score 898; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.8e-77;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QVAFAMVMGTHYSHWPCSCPSKGQDTSEELLRWSTVPPPLEPARNRHPESCRASE 62  
Db 19 QVAFAMVMGTHYSHWPCSCPSKGQDTSEELLRWSTVPPPLEPARNRHPESCRASE 78  
Qy 63 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCHVCVSLQSGHMDPRGNSSELYHNQT 122  
Db 79 DGPLNSRAISPMRYELDRDLNRLPDQLYHARCLCHVCVSLQSGHMDPRGNSSELYHNQT 138  
Qy 123 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 161  
Db 139 VFYRPPCHGEKTHGYCLERRLYRVSLACVCVPRVMG 177

RESULT 10  
US-10-063-598-156  
; Sequence 156, Application US/10063598  
; Publication No. US20030050462A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,598  
; CURRENT FILING DATE: 2002-05-01  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 156  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-063-598-156

Query Match 98.7%; Score 898; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.8e-77;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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, PRIOR APPLICATION NUMBER: PCT/US99/05028
, PRIOR FILING DATE: 1999-03-08
, PRIOR APPLICATION NUMBER: PCT/US99/10733
, PRIOR FILING DATE: 1999-05-14
, PRIOR APPLICATION NUMBER: PCT/US99/31274
, PRIOR FILING DATE: 1999-12-30
, PRIOR APPLICATION NUMBER: PCT/US00/04341
, PRIOR FILING DATE: 2000-02-18
, PRIOR APPLICATION NUMBER: PCT/US00/05601
, PRIOR FILING DATE: 2000-03-01
, PRIOR APPLICATION NUMBER: PCT/US00/05841
, PRIOR FILING DATE: 2000-03-02
, PRIOR APPLICATION NUMBER: PCT/US00/07532
, PRIOR FILING DATE: 2000-03-21
, PRIOR APPLICATION NUMBER: PCT/US00/15264
, PRIOR FILING DATE: 2000-06-02
, PRIOR APPLICATION NUMBER: PCT/US00/23328
, PRIOR FILING DATE: 2000-08-24
, PRIOR APPLICATION NUMBER: PCT/US00/30873
, PRIOR FILING DATE: 2000-11-10
, PRIOR APPLICATION NUMBER: PCT/US00/32678
, PRIOR FILING DATE: 2000-12-01
, PRIOR APPLICATION NUMBER: PCT/US00/34956
, PRIOR FILING DATE: 2000-12-20
, PRIOR APPLICATION NUMBER: PCT/US01/06520
, PRIOR FILING DATE: 2001-02-28
, NUMBER OF SEQ ID NOS: 39
, SEQ ID NO 6
, LENGTH: 177
, TYPE: PRT
, ORGANISM: Homo Sapien
US-09-908-827-6

```

| Query Match           | 98.7%;          | Score 898;                                                   | DB 9;     | Length 177; |
|-----------------------|-----------------|--------------------------------------------------------------|-----------|-------------|
| Best Local Similarity | 100.0%;         | Prod. No. 3.8e-77;                                           |           |             |
| Matches 159;          | Conservative 0; | Mismatches 0;                                                | Indels 0; | Gaps 0;     |
| QY                    | 3               | QVAFLAVMWGTHYSHWPSCCPKSGQDTSSELLRWSTVPVPPLEPARPNRHPSCRASE    | 62        |             |
|                       |                 |                                                              |           |             |
| Db                    | 19              | QVAFLAVMWGTHYSHWPSCCPKSGQDTSSELLRWSTVPVPPLEPARPNRHPSCRASE    | 78        |             |
|                       |                 |                                                              |           |             |
| QY                    | 63              | DGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSQLTGSHMPDRGNSellyhNOT | 122       |             |
|                       |                 |                                                              |           |             |
| Db                    | 79              | DGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSQLTGSHMPDRGNSellyhNOT | 138       |             |
|                       |                 |                                                              |           |             |
| QY                    | 123             | VFYRPPCHGKGGTHKGYCLERRLYRVSLACVCVVRPYMG                      | 161       |             |
|                       |                 |                                                              |           |             |
| Db                    | 139             | VFYRPPCHGKGGTHKGYCLERRLYRVSLACVCVVRPYMG                      | 177       |             |
|                       |                 |                                                              |           |             |

```

RESULT 13
US-10-213-181-18
; Sequence 18, Application US/10213181
; Publication No. US20030054484A1
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods
; FILE OF INVENTION: Related Diseases
; FILE REFERENCE: P1313R17
; CURRENT APPLICATION NUMBER: US/10/213,181
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US/052,594
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: PCT/US00/30873

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: PRIOR FILING DATE: 2000-11-10
: PRIOR APPLICATION NUMBER: US 60/177,118
:
: PRIOR FILING DATE: 2000-01-20
: NUMBER OF SEQ ID NOS: 24
: SEQ ID NO 18
: LENGTH: 177
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-213-181-18

```

|    | Query Match                                                                   | 98.7%; Score 898; DB 9; | Length 177;                     |
|----|-------------------------------------------------------------------------------|-------------------------|---------------------------------|
|    | Best Local Similarity                                                         | 100.0%;                 | Pred. No. 3.e-77;               |
|    | Matches 159; Conservative                                                     | 0;                      | Mismatches 0; Indels 0; Gaps 0; |
| Qy | 3 QVAF <sup>LAWMGTHYTSHPSCCPSKGGDTSEELLRWSTVP</sup> VPPLEPARNHPSERASE 62<br>  |                         |                                 |
| Dd | 19 QVAF <sup>LAWMGTHYTSHPSCCPSKGGDTSEELLRWSTVP</sup> VPPLEPARNHPSERASE 78<br> |                         |                                 |
| Qy | 63 DGPLNSRAISPWRYELDRDLNRLPDQLHYARCLCPHCVSLSQTGSHMDPRGNSELLYHNQT 122<br>      |                         |                                 |
| Dd | 79 DGPLNSRAISPWRYELDRDLNRLPDQLHYARCLCPHCVSLSQTGSHMDPRGNSELLYHNQT 138<br>      |                         |                                 |
| Qy | 123 VFTRPCBGSKGHKGVCYLERRLRYRSLACVCVRPRVMG 161<br>                            |                         |                                 |
| Dd | 139 VFYRRPCBGSKGHKGVCYLERRLRYSVLACVCVRPRVMG 177<br>                           |                         |                                 |

```

RESULT 14
US-10-063-567-156
; Sequence 156, Application US/10063567
; Publication No. US20030069394A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRAN
; TITLE OF INVENTION: ACIDS ENCODING
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/06
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 156
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-567-156

```

```

Query Match          98.7%; Score 898; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.8e-77;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY      3 QVAFAMVMGTTTYSHPWSCCPKSGDTSSELLRWSTVPVPLEPARNRHPESCRASE 62
        |||
Db       19 QVAFAMVMGTTTYSHPWSCCPKSGDTSSELLRWSTVPVPLEPARNRHPESCRASE 78
        |||

QY      63 DGPLNSRAISPWRYELDRDLNRLPDQLYHARCICPHCVSLQTGSHMDPRGNSELLYHNQT 122
        |||
Db       79 DGPLNSRAISPWRYELDRDLNRLPDQLYHARCICPHCVSLQTGSHMDPRGNSELLYHNQT 138
        |||

QY      123 VFYRRPCHEKGTHKGVCLERRLYRVSLACVCVRPRVMG 161
        |||||
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RESULT 15
US-10-063-538-156
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; Sequence 156, Application US/10063538
; Publication No. US20030073208A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,538
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 156
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-538-156

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Query Match      98.7%   Score 898; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.8e-77;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   19 QVAFAMVMGTHYSHWPCSCPSKGQDTSEELLRWSTVPVPPLEPARPNRHPSERASE 78
    |||

Qy   63 DGPLNSRAISPRYELDRDLNRLFDLYHARCLCPHCYSLQGTGSHMDPRGNSSELYHNQT 122
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Db   79 DGPLNSRAISPRYELDRDLNRLFDLYHARCLCPHCYSLQGTGSHMDPRGNSSELYHNQT 138
    |||

Qy   123 VFYRRPCHGEKGTGKGYCLERRLYRVSLACVCVPRVNG 161
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Db   139 VFYRRPCHGEKGTGKGYCLERRLYRVSLACVCVPRVNG 177
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Search completed: May 12, 2003, 02:02:13  
Job time : 31 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 12, 2003, 02:00:49 ; Search time 1762 Seconds  
(without alignments)  
2659.223 Million cell updates/sec

Title: US-10-037-591A-2

Perfect score: 910

Sequence: 1 MYQVAFAMVMTHTYSHW.....ERRLYRVSLACVCRPRVMG 161

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
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Database :

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6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
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38: em.sy.\*  
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40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description        |
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| 1          | 910   | 100.0         | 504    | 6     | AX299773 Sequence  |
| 2          | 910   | 100.0         | 644    | 6     | AX253225 Sequence  |
| 3          | 910   | 100.0         | 644    | 6     | AX365242 Sequence  |
| 4          | 904   | 99.3          | 486    | 9     | AF458059 Homo sapi |
| 5          | 898   | 98.7          | 1320   | 6     | AX092424 Sequence  |
| 6          | 898   | 98.7          | 1320   | 6     | AX164145 Sequence  |
| 7          | 898   | 98.7          | 1320   | 6     | AX180768 Sequence  |
| 8          | 898   | 98.7          | 1335   | 9     | AF305200 Homo sapi |
| 9          | 709   | 77.9          | 985    | 6     | AX299775 Sequence  |
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| 11         | 709   | 77.9          | 1013   | 6     | AX365244 Sequence  |
| 12         | 693   | 76.2          | 1496   | 6     | AX365250 Sequence  |
| 13         | 652   | 71.6          | 462    | 10    | AY034088 Sequence  |
| 14         | 495   | 54.4          | 157910 | 9     | CNS01DTR Human chr |
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| 17         | 430.5 | 47.3          | 160950 | 2     | AC119293 Rattus no |
| c 18       | 314.5 | 34.6          | 170032 | 2     | AC116673 Mus muscu |
| c 19       | 277   | 30.4          | 160950 | 2     | AC119293 Rattus no |
| c 20       | 277   | 30.4          | 171821 | 2     | AC115371 Rattus no |
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| 22         | 167   | 18.4          | 591    | 6     | AX427978 Sequence  |
| 23         | 167   | 18.4          | 1047   | 6     | AX180766 Sequence  |
| 24         | 167   | 18.4          | 1047   | 6     | AX376380 Sequence  |
| 25         | 167   | 18.4          | 1047   | 9     | AF152099 Homo sapi |
| 26         | 167   | 18.4          | 1078   | 9     | AF142410 Homo sapi |
| 27         | 167   | 18.4          | 1177   | 6     | AX223949 Sequence  |
| 28         | 126.5 | 13.9          | 609    | 9     | AF479775 Homo sapi |
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| 30         | 126.5 | 13.9          | 1873   | 9     | AF078238 Homo sapi |
| 31         | 125.5 | 13.8          | 684    | 9     | AF218727 Homo sapi |
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| 35         | 125.5 | 13.8          | 687    | 6     | AX180764 Sequence  |
| 36         | 125.5 | 13.8          | 687    | 6     | AX464312 Sequence  |
| 37         | 125.5 | 13.8          | 687    | 9     | AF152098 Homo sapi |
| 38         | 125.5 | 13.8          | 688    | 9     | AF184969 Homo sapi |
| 39         | 125.5 | 13.8          | 703    | 9     | AF110385 Homo sapi |
| 40         | 125.5 | 13.8          | 711    | 9     | AF212311 Homo sapi |
| 41         | 125.5 | 13.8          | 736    | 6     | AX236262 Sequence  |
| 42         | 125.5 | 13.8          | 1754   | 6     | AX180770 Sequence  |
| 43         | 125.5 | 13.8          | 1754   | 6     | AX358834 Sequence  |
| 44         | 125.5 | 13.8          | 1754   | 6     | AX362327 Sequence  |
| 45         | 124   | 13.6          | 947    | 9     | AF332389 Homo sapi |

# ALIGNMENTS

RESULT 1

Db 439 CTGAGCGCAGCGTGTACCGTGTTCCTTACGCTGTGTGTGTGGCGCCCGCTGTGATG 498

Qy 161 Gly 161  
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Db 499 GGC 501

RESULT 2  
AX253225  
LOCUS AX253225 644 bp DNA linear PAT 05-OCT-2001  
DEFINITION Sequence 22 from Patent WO0168705.  
ACCESSION AX253225  
VERSION AX253225.1 GI:15986362  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Jing, S., Medlock, E., Yeh, R., Silbiger, S.M., Elliot, G.S. and  
Nguyen, H.Q.  
TITLE IL-17 receptor like molecules and uses thereof  
JOURNAL Patent: WO 0168705-A 22 20-SEP-2001;  
Angen Inc. (US)  
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BASE COUNT 144 a 204 c 173 g 123 t

ORIGIN

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Pred. NO.: 5.62e-55 Length: 644  
Score: 910.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

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Qy 21 ProSerCysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTyrSerThr 40  
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Db 219 CCCAGCTGCTGCCCAGCAAAAGGCGAGACACCTCTCAGGAGCTGCTGAGGTGGAGCACT 278  
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Qy 41 ValProValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAla 60  
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Db 279 GTGCCGTGTGCTCCCTAGACCTGCTAGGCCCAACCGCCACCCAGAGTCTCTAGG GCC 338  
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Qy 61 SerGluAspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArg 80  
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Qy 81 AspLeuAsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysVal 100  
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Qy 101 SerLeuGlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsn 120  
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Db 459 AGCCTFACAGACAGCTCCCATCATGACCCCGGGGCACTCGAGCTGCTTACCAAC 518  
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QY 121 GlnThrValPheTyrArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCys 140
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QY 141 LeuGluArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMet 160
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Db 579 CTGGAGCGCAGGCTGTACCGCTTTCTTCTAGCTGTGTGTGGCGCCCGCTGTGATG 638
QY 161 Gly 161
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Db 639 GGC 641

RESULT 3
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LOCUS AX365242 644 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 1 from Patent WO0208285.
ACCESSION AX365242
VERSION AX365242.1 GI:18696995
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Medlock,E., Yeh,R., Silbiger,S.M., Elliot,G.S., Nguyen,H.Q. and
Jing,S.
TITLE IL-17 molecules and uses thereof
JOURNAL Patent: WO 0208285-A 1 31-JAN-2002;
Amgen, Inc. (US)
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Score: 910.00 Matches: 161
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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QY 21 ProSerCysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThr 40
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Db 219 CCCAGCTGCTGCCCGACCAAGGCGAGACACCTCTGAGGAGCTCTGAGGTGGAGCACT 278
QY 41 ValProValProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAla 60
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Db 279 GTGCCGTGCTCCCTAGAGCTCTAGGCCCAACGCCACCCAGAGTCCTGTAGGGCC 338
QY 61 SerGluAspGlyProLeuAsnSerArgAlaLeuSerProTrpArgTyrGluLeuAspArg 80
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Db 339 AGTGAAGATGGACCCCTCAACAGCAGGCGCCATCTCCCTCGGAGATATGAGTTGGACAGA 398
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Db 399 GACTTGAACCGGCTCCCCAGGACCTGTACACACGCCCGTTGCTGTGCTCCGCACTGGCTC 458
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Db 459 AGCTACAGACAGGCTCCACATGGACCCCGGGCAACTCGGAGCTGCTCTACCAAC 518
QY 121 GlnThrValPheTyrArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCys 140
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Db 519 CAGACTGTCTTACCGCGCGCATCCATGGGAGAGGGACCCACAGGGCTACTGC 578
QY 141 LeuGluArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMet 160
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Db 579 CTGGAGCGCAGGCTGTACCGCTTTCTTCTAGCTGTGTGTGGCGCCCGCTGTGATG 638
QY 161 Gly 161
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Db 639 GGC 641

RESULT 4
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LOCUS AF458059 486 bp mRNA linear PRI 15-JAN-2002
DEFINITION Homo sapiens IL25 mRNA, complete cds.
ACCESSION AF458059
VERSION AF458059.1 GI:18034675
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 486)
AUTHORS Fort,M.M., Cheung,J., Yen,D., Li,J., Zurawski,S.M., Lo,S.,
Menon,S., Clifford,T., Hunte,B., Lesley,R., Muchamuel,T.,
Hurst,S.D., Zurawski,G., Leach,M.W., Gorman,D.M. and Rennick,D.M.
TITLE IL-25 induces IL-4, IL-5, and IL-13 and Th2-associated pathologies
in vivo
JOURNAL Immunity 15 (6), 985-995 (2001)
MEDLINE 21629216
PUBMED 11754819
REFERENCE 2 (bases 1 to 486)
AUTHORS Hurst,S.D., Muchamuel,T., Gorman,D.M., Gilbert,J.M., Clifford,T.,
Kwan,S., Menon,S., Seymour,B., Jackson,C., Kung,T., Brieland,J.,
Zurawski,S.M., Chapman,R., Zurawski,G. and Coffman,R.L.
TITLE New IL-17 family members promote Th1 or Th2 responses in the lung:
in vivo function of the novel cytokine IL-25
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 486)
AUTHORS Gilbert,J.M. and Gorman,D.M.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-2001) Genomics, DNAX Research Inc., 901
California Ave., Palo Alto, CA 94304, USA
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Query Match: 99.34% Indels: 0

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Db 61 CCCAGCTGCTCCCCAGCAAGGCGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACT 120
Qy 41 ValProValProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAla 60
Db 121 GTGCTGTGCTCCCTAGAGCTGCTAGGCCCAACCCAGAGTCTCTGTAGGCCC 180
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Db 361 CAGACTGTCTTCTACCGGCGCCATGCCATGGCGAAGAGGCGCACCAAGGCTACTGCG 420
Qy 141 LeuGluArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMet 160
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DEFINITION Sequence 155 from Patent WO0116318.
ACCESSION AX092424
VERSION AX092424.1 GI:13444526
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 155 08-MAR-2001;
Genentech, Inc. (US)
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Qy 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
Db 373 TGCTGCCCCAGCAAGGCGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCT 432
Qy 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62
Db 433 GTGCTCCCTAGAGCTGCTAGGCCCAACCCAGAGTCTCTGTAGGCGCACTGAA 492
Qy 63 AspGlyProLeuAsnSerArgAlaIleSerProTTPArgTyrGluLeuAspArgAspLeu 82
Db 493 GATGACCCCTCAACAGCAGGCGCATCTCCCTGGAGATATGAGTTGGACAGAGACTTG 552
Qy 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102
Db 553 AACCGGCTCCCCAGGACCTGTACCAAGCCCTGTGCTGCTGCGCGCACTGCGTCAGCCTA 612
Qy 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122
Db 613 CAGACAGGCTCCACATGACCCCGGGGCAACTCGGAGCTGCTTACCAACACCACT 672
Qy 123 ValPheTyrArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142
Db 673 GTCTTCTACGCGGCGCATGCCATGGCGAAGAGGCGCACCAAGGCTACTGCTGCGG 732
Qy 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161
Db 733 CGCAGGCTGACCGTGTTCCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 789
RESULT 6
AX164145 LOCUS 1320 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 17 from Patent WO0140465.
ACCESSION AX164145
VERSION AX164145.1 GI:14545087
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Fong,S., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L.,
Hillan,K.J., Tumas,D., Watanabe,C.K., Wood,W.I. and Zhang,Z.
TITLE Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 0140465-A 17 07-JUN-2001;
Genentech, Inc. (US)
FEATURES
source
Location/Qualifiers
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BASE COUNT 280 a 353 c 384 g 303 t
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Pred. No.: 7.6e-54 Length: 1320
Score: 898.00 Matches: 159
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.68% Indels: 0
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Qy 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
Db 373 TGCTGCCCCAGCAAGGCGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCT 432
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|                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                |                 |
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| Qy                     | 63                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | AspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu   | 82              |
| Db                     | 493                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | GATGGACCCCTCAACAGCAGGCGCCATCTCCCCCTGGAGATATAGTTGGACAGAGACTTG   | 552             |
| Qy                     | 83                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu   | 102             |
| Db                     | 553                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | AACCGGGTCCCGCCAGGACCTGTACAGCGCCCGTGTCCCTGTGCGCGCACTGGCTCAGCCTA | 612             |
| Qy                     | 103                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr   | 122             |
| Db                     | 613                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | CAGACAGGCTCCCAATGAGCCCGGGGCAACTCGGAGCTGCTCTACCAACACCACT        | 672             |
| Qy                     | 123                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ValPheTyrArgProCysHisGlyGluCysGlyThrHisLysGlyTyrCysLeuGlu      | 142             |
| Db                     | 673                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | GTCTTCTACAGCGCGCCATGCGCATGGCAGAGGCGACCCACAAAGGGCTACTGCTCGGAG   | 732             |
| Qy                     | 143                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly      | 161             |
| Db                     | 733                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | CGCAGGCTGTACCGTGTCTTCTTAACTGTGTGTGTGTCGGCGCCCGCTGTATGGC        | 789             |
| RESULT                 | 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                |                 |
| LOCUS                  | AF305200                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 1335 bp mRNA linear                                            | PRI 09-JAN-2001 |
| DEFINITION             | Homo sapiens interleukin 17E (IL17E) mRNA, complete cds.                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                |                 |
| ACCESSION              | AF305200                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                |                 |
| VERSION                | AF305200.1                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | GI:11878209                                                    |                 |
| KEYWORDS               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                |                 |
| SOURCE                 | Homo sapiens.                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                |                 |
| ORGANISM               | Homo sapiens                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                |                 |
| REFERENCE              | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.                                                                                                                                                                                                                                                                                                                                                  |                                                                |                 |
| AUTHORS                | 1 (bases 1 to 1335)<br>Lee, J., Ho, W.-H., Maruoka, M., Corpuz, R.T., Baldwin, D.T., Foster, J.S., Goddard, A.D., Yansura, D.G., Vandlen, R.L., Wood, W.I. and Gurney, A.L.                                                                                                                                                                                                                                                                                                   |                                                                |                 |
| TITLE                  | IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog IL-17RH1                                                                                                                                                                                                                                                                                                                                                                                                |                                                                |                 |
| JOURNAL                | J. Biol. Chem. 276 (2), 1660-1664 (2001)                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                |                 |
| MEDLINE                | 21125711                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                |                 |
| PUBMED                 | 11058597                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                |                 |
| REFERENCE              | 2 (bases 1 to 1335)<br>Lee, J., Ho, W.-H., Maruoka, M., Corpuz, R.T., Baldwin, D., Foster, J.S., Goddard, A.D., Yansura, D.G., Vandlen, R.L., Wood, W.I. and Gurney, A.L.                                                                                                                                                                                                                                                                                                     |                                                                |                 |
| AUTHORS                | Direct Submission                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                |                 |
| TITLE                  | Submitted (12-SEP-2000) Molecular Biology, Genentech, 1 DNA Way, South San Francisco, CA 94080, USA                                                                                                                                                                                                                                                                                                                                                                           |                                                                |                 |
| JOURNAL                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                |                 |
| FEATURES               | Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                |                 |
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| BASE COUNT             | 295 a 353 c 384 g 303 t                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                |                 |
| ORIGIN                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                |                 |
| Alignment Scores:      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                                |                 |
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| Percent Similarity:    | 100.00%                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Conservatives:                                                 | 0               |
| Best Local Similarity: | 100.00%                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Mismatches:                                                    | 0               |

Query Match: 98.68% Indels: 0 Gaps: 0

DB: 9

US-10-037-591a-2 (1-161) x AF305200 (1-1335)

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QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42  
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 DEFINITION Sequence 3 from Patent WO0179288.  
 ACCESSION AX299775  
 VERSION AX299775.1 GI:17129296  
 KEYWORDS  
 SOURCE unidentified.  
 ORGANISM unidentified.  
 1 unclassified.

REFERENCE  
 1 Hurst,S.D., Zurawski,S.M. and Rennick,D.M.  
 Cytokine uses; compositions; methods  
 Patent: WO 0179288-A 3 25-OCT-2001;  
 SCHERING CORPORATION (US)  
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BASE COUNT 199 a 296 c 268 g 222 t  
 ORIGIN

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Score: 709.00 Matches: 129  
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US-10-037-591a-2 (1-161) x AX299775 (1-985)

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QY 93 ArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArgGly 112  
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QY 113 AsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArgProCysHisGlyGlu 132  
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 Db 361 ACTCCGTCCCACTTACCACACAGCAGCTCTTACCCGGCGCCATGCCATGGTGAG 420

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QY 153 ValCysValArgProArgValMet 160  
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RESULT 10  
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 DEFINITION Mus musculus IL25 mRNA, complete cds.  
 ACCESSION AF458060  
 VERSION AF458060.1 GI:18034677  
 KEYWORDS  
 SOURCE Mus musculus.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 985)  
 AUTHORS Hurst,S.D., Muchamuel,T., Gorman,D.M., Gilbert,J.M., Clifford,T.,  
 Kwan,S., Menon,S., Seymour,B., Jackson,C., Kung,T., Brieland,J.,  
 Zurawski,S.M., Chapman,R., Zurawski,G. and Coffman,R.L.  
 New IL-17 family members promote Th1 or Th2 responses in the lung:  
 In vivo function of the novel cytokine IL-25

TITLE Immunity 15 (6), 985-995 (2001)  
 JOURNAL  
 MEDLINE 21629216  
 PUBMED 11754819  
 REFERENCE 2 (bases 1 to 985)  
 AUTHORS Hurst,S.D., Muchamuel,T., Gorman,D.M., Gilbert,J.M., Clifford,T.,  
 Kwan,S., Menon,S., Seymour,B., Jackson,C., Kung,T., Brieland,J.,  
 Zurawski,S.M., Chapman,R., Zurawski,G. and Coffman,R.L.  
 New IL-17 family members promote Th1 or Th2 responses in the lung:  
 In vivo function of the novel cytokine IL-25

TITLE Unpublished  
 JOURNAL 3 (bases 1 to 985)  
 REFERENCE  
 AUTHORS Gilbert,J.M. and Gorman,D.M.

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
CDS  
BASE COUNT  
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Pred. No.:  
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Percent Similarity:  
Best Local Similarity:  
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Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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Medlock, E., Yeh, R., Silbiger, S.M., Elliot, G.S., Nguyen, H.Q. and  
Jing, S.  
11-17 molecules and uses thereof  
Patent: WO 0208285-A 3 31-JAN-2002;  
Angen, Inc. (US)  
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DEFINITION Sequence 9 from Patent WO200285.
ACCESSION AX365250
VERSION AX365250.1 GI:18696999
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SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Medlock, E., Yeh, R., Silbiger, S.M., Elliot, G.S., Nguyen, H.Q. and
Jing, S.
TITLE 11-17 molecules and uses thereof
JOURNAL Patent: WO 0208285-A 9 31-JAN-2002;
Angen, Inc. (US)
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QY 18 -----SerHisTrpProSerCysProSerLysGlyGlnAspThrSerGluGlu 34
Db 550 GAGGGCTGCAGTCACTTGCACGCTGCTGCCCCAGCAAGAGCAAGAACCCCGGAGGAG 609
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QY 95 LeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArgGlyAsnSer 114
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QY 135 ThrHisLysGlyTyrCysLeuGluArgArgLeuTyrArgValSerLeuAlaCysValCys 154
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ACCESSION AY034088
VERSION AY034088.1 GI:17266279
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SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 462)
AUTHORS Pan, G., French, D., Mao, W., Maruoka, M., Risser, P., Lee, J.,
Foster, J., Aggarwal, S., Nicholes, K., Guillet, S., Schow, P. and
Gurney, A.L.
TITLE Forced expression of murine IL-17E induces growth retardation,
jaundice, a Th2-biased response, and multiorgan inflammation in
mice
JOURNAL J. Immunol. 167 (11), 6559-6567 (2001)
MEDLINE 21571724
PUBMED 11714825
REFERENCE 2 (bases 1 to 462)
AUTHORS Pan, G., Mao, W., Maruoka, M., French, D., Risser, P., Lee, J.,
Foster, J., Aggarwal, S., Nicholes, K., Guillet, S., Schow, P. and
Gurney, A.L.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-2001) Molecular Biology, Genentech, 1 DNA Way,
South San Francisco, CA 94080, USA
FEATURES
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QY 58 CysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGlu 77
Db 148 TGCAGGGCCAGCAAGGATGCGCCCTCAACAGCAGGCGCATCTCTCTTGGAGCTATGAG 207
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Search completed: May 12, 2003, 02:36:25  
Job time : 1817 secs

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Db 375 CTGCGCAGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 434
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Db 594 ATC-----ACCATCCGGTGGGCTGCACCTGGCGTG 623

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US-08-514-014-11
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; Patent No. 5707829
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/514,014
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G16000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
```

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; LOCATION: 86...544
US-08-514-014-11
Alignment Scores:
Pred. No.: 0.00192 Length: 813
Score: 120.50 Matches: 40
Percent Similarity: 40.79% Conservative: 22
Best Local Similarity: 26.32% Mismatches: 49
Query Match: 13.24% Indels: 41
DB: 1 Gaps: 7

US-10-037-591A-2 (1-161) x US-08-514-014-11 (1-813)
QY 15 HisThrTyrSerHisTrpProSerCysProSerLysGlyGlnAspThrSerGluGlu 34
Db 167 CATACTTTTTTCCAAAAGCCTGAGAGTTGCCCG----- 199
QY 35 LeuLeuArgTrpSerThrValProValPro-----ProLeuGluProAlaArg 50
Db 200 -----CCTGGCCAGGAGGTAGTATGAAGCTTGACATTGGGCATC 238
QY 51 ProAsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAla 70
Db 239 ATCAAT-----GAAAACAGCGCGTTTCCATGTACGTAAACATCGAGAGCGCGTCC 289
QY 71 IleSerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyr 90
Db 290 ACCTCCCGCTGGAATTACACTGTCACTTGGGAGCCCCAACCGGTACCCCTCGGAAGTTGTA 349
QY 91 HisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspPro 110
Db 350 CAGGCCCCAGTGTAGGAACCTTCATGATCAATCAATGCTCAA----- 388
QY 111 ArgGlyAsnSerGluLeuLeuTyrHisAsn-----GlnThrValPheTyr 125
Db 389 ---GGAAGGAAGACATCTCCATGAATTCGTTCCCATCCAGCAAGAGACCCCTGTCGTC 445
QY 126 ArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGluArgLeu 145
Db 446 CGGAGGAAG-----CACCAAGGCTGCTCTCTTTTCCAGTTGGAGAGGTGCTG 496
QY 146 TyrArgValSerLeuAlaCysValCysValArgPro 157
Db 497 -----GTGACTGTGTGCTGCACCTGCGTCACCCCT 526

RESULT 3
US-08-833-823-11
; Sequence 11, Application US/08833823
; Patent No. 5969093
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,823
; FILING DATE: 10-APR-1997
; CLASSIFICATION: 530
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PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/077,203
  FILING DATE: 14-JUN-1993
  ATTORNEY/AGENT INFORMATION:
    NAME: Ching, Edwin P.
    REGISTRATION NUMBER: 34,090
  REFERENCE/DOCKET INFORMATION:
    TELEPHONE: 415-852-9196
    TELEFAX: 415-496-1200
  INFORMATION FOR SEQ ID NO: 7:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 510 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      FEATURE:
        NAME/KEY: CDS
        LOCATION: 43..507
US-08-432-994A-7

Alignment Scores:
Pred. No.: 0.269 Length: 510
Score: 96.50 Matches: 34
Percent Similarity: 37.12% Conservative: 15
Best Local Similarity: 25.76% Mismatches: 58
Query Match: 10.60% Indels: 25
DB: 4 Gaps: 5

US-10-037-591A-2 (1-161) x US-08-432-994A-7 (1-510)
QY 45 ProLeuGluProAlaArgProAsnArgHisProGluSerCys----- 58
DB 124 CCACGAATCCAGGATGCCAATCTCTGAGGACAGAACTTCCCGGAGCTGTGATGGTC 183
QY 59 -----ArgAlaSerGluAspGlyProLeuAsnSer----- 68
DB 184 AACCTGACATCCATAACCGGAATACCAATCCCAAGGTCCTCAGATTACTAC 243
QY 69 ---ArgAlaIleSerProTrpArgTyrGluLeuAspArgAsnArgLeuProGln 87
DB 244 AACCGATCCACCTACCTTGGAAATCTCCACCGCAATGAGGACCTGAGAGATATCCCTCT 303
QY 88 AspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHis 107
DB 304 GTGATCTGGGGGCAAG-----TGCCGCCACTTGGGCTGCATCAACGCTGATGGGAC 357
QY 108 MetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArg 127
DB 358 GTGGACTACCATCACTCTGCTCCCATCCAGCAAGAGATCTGCTGCTGCGCAGGGAG 417
QY 128 ProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyrArg 147
DB 418 COTCCACAC-----TGCCCCCAACTCTCTCCGGCTGAGAGATACTG----- 459
QY 148 ValSerLeuAlaCysValCysValArgProArgVal 159
DB 460 GTGCTGGGGCTGCACCTGTGTCTACCCCGGATTGTC 495

RESULT 7
US-08-477-674-9/c
  Sequence 9, Application US/08477674
  Patent No. 5644035
  GENERAL INFORMATION:
    APPLICANT: Koths, Kirston E.
    APPLICANT: Halenbeck, Robert F.
    APPLICANT: Taylor, Eric W.
    APPLICANT: Wang, Alice M.
    APPLICANT: Caspitt, Clayton L.
  TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein
  NUMBER OF SEQUENCES: 11
  CORRESPONDENCE ADDRESS:
    ADDRESS: Cetus Oncology Corporation
    STREET: 1400 Fifty-Third Street
    CITY: Emeryville
    STATE: CA
    COUNTRY: USA
    ZIP: 94608
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION NUMBER: US/08/477,674
    FILING DATE: 07-JUN-1995
    CLASSIFICATION: 530
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/08/316,714
      FILING DATE:
      APPLICATION NUMBER: US/07/961,404
      FILING DATE: 15-OCT-1992
      ATTORNEY/AGENT INFORMATION:
        NAME: Goldman, Kenneth M.
        REGISTRATION NUMBER: 34,174
        REFERENCE/DOCKET NUMBER: 2595.1
        TELECOMMUNICATION INFORMATION:
          TELEPHONE: (510) 420-3152
          TELEFAX: (510) 658-5470
          TELEX: N/A
      INFORMATION FOR SEQ ID NO: 9:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 2285 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
          MOLECULE TYPE: DNA (genomic)
US-08-477-674-9

Alignment Scores:
Pred. No.: 4.45 Length: 2285
Score: 93.50 Matches: 44
Percent Similarity: 30.23% Conservative: 8
Best Local Similarity: 25.58% Mismatches: 42
Query Match: 10.27% Indels: 78
DB: 1 Gaps: 9

US-10-037-591A-2 (1-161) x US-08-477-674-9 (1-2285)
QY 9 AlaMetValMetGlyThrHisThrTyrSer-His---TrrProSerCysCysProSerLy 27
DB 799 TCCCTGACCATGGGCACACACTCAGCATCCACACTCATGTGTGACATTCGTCGCCGGCTCC 740
QY 27 sGlyGlnAspThrSerGluGluLeuLeuArgTrrSerThrValProValProPro----- 45
DB 739 T-----TCCACAGGGCTGGGCTCCAGGTG 713
QY 46 -----LeuGluProAlaArgPro----- 51
DB 712 GCAGTCAGGATGACCTGTGGCCACAGACGCCAGGGCGTCTCGCCCTGCACATTACG 653
QY 52 -----AsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnse 68
DB 652 CTGATGGACAGGTGCGAGCCCGCTGGCTGTCAAAGATCTGGCCAGGGCTCCGAGA-- 595
QY 68 rArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAs 88
DB 594 -----GCTCCCTGGAGA----- 583
QY 88 pleuTyrHisAlaArgCysLeuCys-----ProHis----- 98
DB 582 -----GCTCCAGGGTGTGGGTGCTCTGTTTCATTGTTGTCAGACACACACAGCTCT 530
QY 99 -----CysValSerLeuGlnThrGlySerHisMetAspProArgGlyAs 113

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SEQUENCE CHARACTERISTICS:  
LENGTH: 2285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-316-714-9

Alignment Scores:  
Pred. No.: 4.45 Length: 2285  
Score: 93.50 Matches: 44  
Percent Similarity: 30.23% Conservatives: 8  
Best Local Similarity: 25.58% Mismatches: 42  
Query Match: 10.27% Indels: 78  
DB: 2 Gaps: 9

US-10-037-591A-2 (1-161) x US-08-316-714-9 (1-2285)

Qy 9 AlaMetValMetGlyThrHisThrTyrSer-His---TTPProSerCysCysProSerLy 27  
Db 799 TCCCTGACCATGGGCACACACTCAGCATTCATGTCATGTCGCGGCTCC 740  
Qy 27 sGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValProValProPro----- 45  
Db 739 T-----TCCACAGGCGCTGGGCTCCAGGTTG 713  
Qy 46 -----LeuGluProAlaArgPro----- 51  
Db 712 GCAGTCAGGATGACCGTGTGGCCACAGAGCCGCGCTCTCCCTTCACATTCACG 653  
Qy 52 -----AsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSe 68  
Db 652 CTGATGGACAGTCCGACCGCGCTGGTGTCAAGATCTGGCCAGGCGCTCCGAGA-- 595  
Qy 68 rArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAs 88  
Db 594 -----GCTCCCTGGAGA----- 583  
Qy 88 pLeuTyrHisAlaArgCysLeuCys-----ProHis----- 98  
Db 582 -----GGTCCAGGATGGGCTGCTCTGTTTCATTTGTCACACACACACGCGTCT 530  
Qy 99 -----CysValSerLeuGlnThrGlySerHisMetAspProArgGlyAs 113  
Db 529 CTCCTGCTCCACTTCTCTTCAGCCAGCCAGGACTTCAGTCGCGCA----- 478  
Qy 113 nSerGluLeuTyrHisAsnGlnThrValPheTyrArgProCysHisGlyGluLy 133  
Db 477 -----GTGAGGCGCTCGGTTCCCGTGCACCTGGACCTCG 446  
Qy 133 sGlyThrHisLysGlyTyrCysLeuGluArgArg 144  
Db 445 TCCAGCATGATGGGCGCTGATCTTGGCCCGAAG 412

RESULT 10  
US-08-473-673-9/c  
Sequence 9, Application US/08473673  
Patent No. 6069127  
GENERAL INFORMATION:  
APPLICANT: Koths, Kirston E.  
APPLICANT: Halenbeck, Robert F.  
APPLICANT: Taylor, Eric W.  
APPLICANT: Wang, Alice M.  
APPLICANT: Caspitt, Clayton L.  
TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cetus Oncology Corporation  
STREET: 1400 Fifty-Third Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/473,673  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/316,714  
FILING DATE: 29-SEP-1994  
APPLICATION NUMBER: US/07/961,404  
FILING DATE: 15-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Kenneth M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 2595.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 420-3152  
TELEFAX: (510) 658-5470  
TELEX: N/A

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-473-673-9

Alignment Scores:  
Pred. No.: 4.45 Length: 2285  
Score: 93.50 Matches: 44  
Percent Similarity: 30.23% Conservatives: 8  
Best Local Similarity: 25.58% Mismatches: 42  
Query Match: 10.27% Indels: 78  
DB: 2 Gaps: 9

US-10-037-591A-2 (1-161) x US-08-473-673-9 (1-2285)

Qy 9 AlaMetValMetGlyThrHisThrTyrSer-His---TTPProSerCysCysProSerLy 27  
Db 799 TCCCTGACCATGGGCACACACTCAGCATTCATGTCATGTCGCGGCTCC 740  
Qy 27 sGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValProValProPro----- 45  
Db 739 T-----TCCACAGGCGCTGGGCTCCAGGTTG 713  
Qy 46 -----LeuGluProAlaArgPro----- 51  
Db 712 GCAGTCAGGATGACCGTGTGGCCACAGAGCCGCGCTCTCCCTTCACATTCACG 653  
Qy 52 -----AsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSe 68  
Db 652 CTGATGGACAGTCCGACCGCGCTGGTGTCAAGATCTGGCCAGGCGCTCCGAGA-- 595  
Qy 68 rArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAs 88  
Db 594 -----GCTCCCTGGAGA----- 583  
Qy 88 pLeuTyrHisAlaArgCysLeuCys-----ProHis----- 98  
Db 582 -----GGTCCAGGATGGGCTGCTCTGTTTCATTTGTCACACACACACGCGTCT 530  
Qy 99 -----CysValSerLeuGlnThrGlySerHisMetAspProArgGlyAs 113  
Db 529 CTCCTGCTCCACTTCTCTTCAGCCAGCCAGGACTTCAGTCGCGCA----- 478  
Qy 113 nSerGluLeuTyrHisAsnGlnThrValPheTyrArgProCysHisGlyGluLy 133  
Db 477 -----GTGAGGCGCTCGGTTCCCGTGCACCTGGACCTCG 446

QY 133 sGlyThrHisLysGlyTyrCysLeuGluArg 144  
Db 445 TCCAGCATGATGGGCGCTGATCTTGGCCGAAGG 412

## RESULT 11

US-09-795-691-1/c  
; Sequence 1, Application US/09795691  
; Patent No. 6465230  
; GENERAL INFORMATION:  
; APPLICANT: Meyers, Rachel  
; TITLE OF INVENTION: 27411, A No. 6465230el Human PCP Synthase  
; FILE REFERENCE: 35800/209284  
; CURRENT APPLICATION NUMBER: US/09/795,691  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/185,517  
; PRIOR FILING DATE: 2000-02-28  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2686  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (315)...(1985)  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(2686)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-795-691-1

Alignment Scores:  
Pred. No.: 6.27 Length: 2686  
Score: 93.00 Matches: 32  
Percent Similarity: 38.24% Conservative: 7  
Best Local Similarity: 31.37% Mismatches: 32  
Query Match: 10.22% Indels: 31  
Gaps: 4

US-10-037-591A-2 (1-161) x US-09-795-691-1 (1-2686)

QY 13 GlyThrHisThrTyrSerHisThrProSerCysPro----- 25  
Db 577 GGAACCGGTTTCTGATCCACTGGAACCGGTCGACCGCTTCTGGACACAGGCAGCAAGT 518  
QY 26 -----SerLysGlyGlnAspThrSerGlu 34  
Db 517 GGGAGGTGACCTGGGACACAGCTGGGACACAGCAAGGAGCAATACAGCCATGGTGAC 458  
QY 35 LeuLeuArgTrpSerThrValProValPro-----Pro 45  
Db 457 CTCCTGCGCTGGCGGTCGCGGTTCTGCGGAGCGGTCGGACAGCGCTCCAGGAGCGCG 398  
QY 46 LeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGluAspGlyPro 65  
Db 397 GCCAGCCCTGGCGGCGGACGAGGAGGAGGAGGAGT---CGCCTCCAGAACACGGGTGCC 341  
QY 66 LeuAsnSerArgAlaIleSer-ProTrpArgTyrGluLeuAspArgAspLeuAsnArgIle 85  
Db 340 GCCGAGCTGCGCGCGCCACCGCCATGAGAG-----CTCGCGGACGCGGTGGTGGT 287  
QY 85 uPro 86  
Db 286 CCCT 283

## RESULT 12

US-08-432-994A-3  
; Sequence 3, Application US/08432994A  
; Patent No. 6274711  
; GENERAL INFORMATION:  
; APPLICANT: Golstein, Pierre  
; APPLICANT: Rouvier, Eric  
; APPLICANT: Fossiez, Francois  
; APPLICANT: Lebecque, Serge J.E.

APPLICANT: Djossou, Odile  
APPLICANT: Banchereau, Jacques  
TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND  
TITLE OF INVENTION: RELATED REAGENTS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432,994A  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/250,846  
FILING DATE: 27-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/177,747  
FILING DATE: 05-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/077,203  
FILING DATE: 14-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0388K3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 456 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..453  
US-08-432-994A-3  
Alignment Scores:  
Pred. No.: 0.583 Length: 456  
Score: 92.50 Matches: 31  
Percent Similarity: 44.64% Conservative: 19  
Best Local Similarity: 27.68% Mismatches: 43  
Query Match: 10.16% Indels: 19  
Gaps: 5  
US-10-037-591A-2 (1-161) x US-08-432-994A-3 (1-456)  
QY 52 AsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIle 71  
Db 151 AACTGGATACCTAGTTCTAAAGGGCTTCAGAC-----TACTACATAGATCTACG 201  
QY 72 SerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrHis 91  
Db 202 TCTCTGGACTCTCCATCGCAATGAAGATCAAGATAGATATCCCTCTGTGATTGGAA 261  
QY 92 AlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArg 111  
Db 262 GCAAAGTGTGCTACTTAGGATGTGTTAATGCTGAT----- 297  
QY 112 GlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArgProCys----- 129

Db 298 GGAATGTAGAC-----TACCACATGAAGTCCAGTCCCTATCCAAACAAGAGATTCTTAGTG 351  
QY 130 -----HisGlyGluLysGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyrArg 147  
Db 352 GTGCGCAAGGGCATCAACCCCTGCCCCCTAATTCATTAGGCTAGAGAAGATGCTA----- 405  
QY 148 ValSerLeuAlaCysValCysValArgProArgVal 159  
Db 406 GTGAGTGTAGGCTGCACATCGCTTACTCCCATGTT 441  
RESULT 13  
; Sequence 5, Application US/09034810  
; Patent No. 6043344  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: Kelleher, Kerry  
; APPLICANT: Carlin, McKeough  
; APPLICANT: Goldman, Samuel  
; APPLICANT: Pittman, Debra  
; APPLICANT: Mi, Sha  
; APPLICANT: Neben, Steven  
; APPLICANT: Giannotti, JoAnn  
; APPLICANT: Golden/Fleet, Margaret  
; TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/034,810  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/685,239  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A. 32,724  
; REGISTRATION NUMBER: G15262  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 459 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; NAME/KEY: CDS  
; LOCATION: 1..453  
US-09-034-810-5

Alignment Scores:  
Pred. No.: 0.589 Length: 459  
Score: 92.50 Matches: 31  
Percent Similarity: 44.64% Conservative: 19  
Best Local Similarity: 27.68% Mismatches: 43  
Query Match: 10.16% Indels: 19  
DB: 3 Gaps: 5

US-10-037-591A-2 (1-161) x US-09-034-810-5 (1-459)  
QY 52 AsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIle 71  
Db 151 AACTGGAATACCAAGTCTCTAAAGGGCTTCAGAC-----TACTACAATAGATCTACG 201  
QY 72 SerProTyrArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrHis 91  
Db 202 TCTCTTGGACCTCTCCATCGCATGAAGATCAAGATAGATATCCCTCTGTGATTGGAA 261  
QY 92 AlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArg 111  
Db 262 GCAAGTGTGCTACTTAGGATGTGTTAATGCTGAT----- 297  
QY 112 GlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArgProCys----- 129  
Db 298 GGAATGTAGAC-----TACCACATGAAGTCCCTATCCAAACAAGAGATTCTTAGTG 351  
QY 130 -----HisGlyGluLysGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyrArg 147  
Db 352 GTGCGCAAGGGCATCAACCCCTGCCCTAATTCATTAGGCTAGAGAAGATGCTA----- 405  
QY 148 ValSerLeuAlaCysValCysValArgProArgVal 159  
Db 406 GTGAGTGTAGGCTGCACATCGCTTACTCCCATGTT 441

RESULT 14  
US-08-685-239-5  
; Sequence 5, Application US/08685239  
; Patent No. 6074849  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: Kelleher, Kerry  
; APPLICANT: Carlin, McKeough  
; APPLICANT: Goldman, Samuel  
; APPLICANT: Pittman, Debra  
; APPLICANT: Mi, Sha  
; APPLICANT: Neben, Steven  
; APPLICANT: Giannotti, JoAnn  
; APPLICANT: Golden/Fleet, Margaret  
; TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,239  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; REFERENCE/DOCKET NUMBER: G15262  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 459 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO

FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..453  
US-08-685-239-5

## Alignment Scores:

Pred. No.: 0.589 Length: 459  
Score: 92.50 Matches: 31  
Percent Similarity: 44.64% Conservative: 19  
Best Local Similarity: 27.68% Mismatches: 43  
Query Match: 10.16% Indels: 19  
DB: 3 Gaps: 5

US-10-037-591A-2 (1-161) x US-08-685-239-5 (1-459)

Qy 52 AsnArgHisProGluSerCysArgAlaSerGluAspGlyProLeuAsnSerArgAlaIle 71  
Db 151 AACGGGAATACCGCTTAAAGGGCTTCAGAC-----TACTACAATAGATCTACG 201  
Qy 72 SerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuProGlnAspLeuTyrHis 91  
Db 202 TCTCTGGACTCCATCGCAATGAAGATCAAGATAGATATCCCTCTGTGATTGGAA 261  
Qy 92 AlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySerHisMetAspProArg 111  
Db 262 GCAAGAGTCGCTACTTAGGATGTGTTAATGCTGAT----- 297  
Qy 112 GlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArgArgProCys----- 129  
Db 298 GGGAAATGAGAC-----TACCACATGAACCTCAGTCCTATCCACACAGAGATCTAGT 351  
Qy 130 -----HisGlyGluGlyGlyThrHisGlyGlyTyrCysLeuGluArgArgLeuTyrArg 147  
Db 352 GTGCGCAAGGCGCATCAACCCCTGCCCTAATTCATTAGGCTAGAGAAGATGCTA----- 405  
Qy 148 ValSerLeuAlaCysValCysValArgProArgVal 159  
Db 406 GTGACTGTAGGCTGCACATCGCTTACCTCCCATTTGT 441

## RESULT 15

US-09-034-810-3

Sequence 3, Application US/09034810

Patent No. 6043344

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Mi, Sha

APPLICANT: Neben, Steven

APPLICANT: Giannotti, JoAnn

APPLICANT: Golden Fleet, Margaret

TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/034,810

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/685,239

FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION/DOCKET NUMBER: 32,724

REFERENCE/DOCKET NUMBER: GI5262

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 461 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 6..455

US-09-034-810-3

## Alignment Scores:

Pred. No.: 0.841 Length: 461  
Score: 91.00 Matches: 36  
Percent Similarity: 44.36% Conservative: 23  
Best Local Similarity: 27.07% Mismatches: 52  
Query Match: 10.00% Indels: 23  
DB: 3 Gaps: 6

US-10-037-591A-2 (1-161) x US-09-034-810-3 (1-461)

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Db 58 CGGTACTCATCCCTCAAAAGTTGAGTGTCTCCAAACCGCGAGGCCCAATACCTTTCTCCAGA 117  
Qy 52 -----AsnArgHisProGluSerCysArgAlaSerGluAspGly 64  
Db 118 ACGTGAAGGTCAACCTGAAAGTCAATCACTCCCTT-AGCTCAAAAGCGAGCTCGAGAAGG 176  
Qy 65 ProLeuAsn-----SerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu 82  
Db 177 CCCTCAGATTACCTCAACCGTTCACCTTCCACTTCGACTCTGAGCGCAATGAGGACCT 236  
Qy 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102  
Db 237 GATAGATATCCTTCTGTGATCTGGGAGGCACAGTCCCGCCACAGCGCTGTCTCAACGCT 296  
Qy 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122  
Db 297 GAG-----GGGAAGTTGGACCCACCATGAATTCGTCTCATCCAGCAAGAGATACTA 350  
Qy 123 ValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142  
Db 351 GTCCTGAGAGAGGAGCCCT-----GAGAAGTCCCTTCACT---TTCCGGGTGGAG 398  
Qy 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysVal 155  
Db 399 AAGATGCTG-----GTGGCGGTGGGCTGCACCTGCGTT 431

Search completed: May 12, 2003, 02:54:31  
Job time : 47 secs



GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 12, 2003, 02:02:59 ; Search time 98 Seconds  
(without alignments)  
2041.587 Million cell updates/sec

Title: US-10-037-591A-2  
Perfect score: 910  
Sequence: 1 MYQVAFAMVGMGHTTYSHW.....ERRLYRVSLACVCRVRVMG 161

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 783854 seqs, 621352466 residues

Total number of hits satisfying chosen parameters: 1567708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2\_1/USP70\_spool/US10037591/runat\_06052003\_123155\_22331/app.query.fasta\_1.327  
-DB=PublishedApplications\_NA -QFM=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10037591@cgn1.1.91@runat\_06052003\_123155\_22331  
-NCPU=6 -ICPU=3 -NO\_XLPXY -NO\_MMWP -LARGQUERY -NEG\_SCORES=0 -WAIT -LONLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 910   | 100.0       | 644    | 10 | US-09-886-404-1   |
| 2          | 898   | 98.7        | 1320   | 9  | US-09-874-503-5   |
| 3          | 898   | 98.7        | 1320   | 9  | US-10-000-157-5   |
| 4          | 898   | 98.7        | 1320   | 9  | US-10-063-547-155 |

|    |     |      |      |    |                   |
|----|-----|------|------|----|-------------------|
| 5  | 898 | 98.7 | 1320 | 9  | US-09-747-259-5   |
| 6  | 898 | 98.7 | 1320 | 9  | US-10-063-616-155 |
| 7  | 898 | 98.7 | 1320 | 9  | US-10-063-502-155 |
| 8  | 898 | 98.7 | 1320 | 9  | US-10-063-518-155 |
| 9  | 898 | 98.7 | 1320 | 9  | US-10-063-598-155 |
| 10 | 898 | 98.7 | 1320 | 9  | US-10-227-693-155 |
| 11 | 898 | 98.7 | 1320 | 9  | US-09-908-827-5   |
| 12 | 898 | 98.7 | 1320 | 9  | US-10-213-181-17  |
| 13 | 898 | 98.7 | 1320 | 9  | US-10-063-567-155 |
| 14 | 898 | 98.7 | 1320 | 9  | US-10-063-599-155 |
| 15 | 898 | 98.7 | 1320 | 9  | US-10-212-912-17  |
| 16 | 898 | 98.7 | 1320 | 9  | US-10-213-044-17  |
| 17 | 898 | 98.7 | 1320 | 9  | US-10-063-595-155 |
| 18 | 898 | 98.7 | 1320 | 12 | US-10-006-867-155 |
| 19 | 709 | 77.9 | 1013 | 10 | US-09-886-404-3   |
| 20 | 693 | 76.2 | 1496 | 10 | US-09-886-404-9   |
| 21 | 167 | 18.4 | 594  | 10 | US-09-854-280-17  |
| 22 | 167 | 18.4 | 594  | 10 | US-09-854-208-17  |
| 23 | 167 | 18.4 | 1047 | 9  | US-09-874-503-3   |
| 24 | 167 | 18.4 | 1047 | 9  | US-10-000-157-3   |
| 25 | 167 | 18.4 | 1047 | 9  | US-10-036-041-10  |
| 26 | 167 | 18.4 | 1047 | 9  | US-09-747-259-3   |
| 27 | 167 | 18.4 | 1047 | 9  | US-10-035-855-10  |
| 28 | 167 | 18.4 | 1047 | 9  | US-10-174-590-447 |
| 29 | 167 | 18.4 | 1047 | 9  | US-10-176-758-447 |
| 30 | 167 | 18.4 | 1047 | 9  | US-10-175-737-447 |
| 31 | 167 | 18.4 | 1047 | 9  | US-10-173-706-447 |
| 32 | 167 | 18.4 | 1047 | 9  | US-10-175-738-447 |
| 33 | 167 | 18.4 | 1047 | 9  | US-10-175-752-447 |
| 34 | 167 | 18.4 | 1047 | 9  | US-10-176-482-447 |
| 35 | 167 | 18.4 | 1047 | 9  | US-10-176-757-447 |
| 36 | 167 | 18.4 | 1047 | 9  | US-10-176-913-447 |
| 37 | 167 | 18.4 | 1047 | 9  | US-10-180-552-447 |
| 38 | 167 | 18.4 | 1047 | 9  | US-10-180-557-447 |
| 39 | 167 | 18.4 | 1047 | 9  | US-09-931-836-10  |
| 40 | 167 | 18.4 | 1047 | 9  | US-10-173-700-447 |
| 41 | 167 | 18.4 | 1047 | 9  | US-10-174-572-447 |
| 42 | 167 | 18.4 | 1047 | 9  | US-10-174-579-447 |
| 43 | 167 | 18.4 | 1047 | 9  | US-10-174-582-447 |
| 44 | 167 | 18.4 | 1047 | 9  | US-10-174-588-447 |
| 45 | 167 | 18.4 | 1047 | 9  | US-10-175-739-447 |

ALIGNMENTS

RESULT 1  
US-09-886-404-1  
; Sequence 1, Application US/09886404  
; Patent No. US20020037524A1  
; GENERAL INFORMATION:  
; APPLICANT: Medlock, Eugene  
; APPLICANT: Yeh, Richard  
; APPLICANT: Silbiger, Scott M.  
; APPLICANT: Elliott, Gary S.  
; APPLICANT: Nguyen, Hung Q.  
; APPLICANT: Jing, Shuqian  
; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof  
; FILE REFERENCE: 01017/37128B  
; CURRENT APPLICATION NUMBER: US/09/886,404  
; CURRENT FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 09/810,384  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/266,159  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 60/213,125  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 644  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

[illegible]

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; SEQ ID NO 5
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-874-503-5

Alignment Scores:
Pred. No.: 4.85e-92 Length: 1320
Score: 898.00 Matches: 159
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.68% Indels: 0
DB: 9 Gaps: 0

US-10-037-591A-2 (1-161) x US-09-874-503-5 (1-1320)

Qy 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22
Db 313 CAGGTGGTGTGCTTCTGGCAATGCTATGGGAACCCACACCTACAGCCACTGGCCAGC 372
Qy 23 CysCysProSerLysGlyClnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
Db 373 TGCTCCCCAGCAAGGCGAGACACCTCTGAGGAGCTGCTGAGTGAGCACTGTGCCT 432
Qy 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62
Db 433 GTGCCTCCCTAGAGCCTGCTAGGCCCAACCCGCCACAGAGTCTGTAGGCCAGTGAA 492
Qy 63 AspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu 82
Db 493 GATGACGCCCTCAACAGCAGGCGCCATCTCCCTCGAGATATGAGTTGGACAGACATTG 552
Qy 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102
Db 553 AACCGGCTCCCCAGGAGCTGTACACACCCCGTTCCTGTGCGCCGCACTGGCTGACCTA 612
Qy 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122
Db 613 CAGACAGGCTCCCATATGAGCCCGGGGCACTCGGAGTGTCTTACCACAAACAGACT 672
Qy 123 ValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142
Db 673 GTCTTCTACAGCGGCCATGCCATGCGGAGAGGCCACCCACAAAGGCTACTGCGCTGGAG 732
Qy 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161
Db 733 GCAGGCTGTACCGGTGTTCTTACCTTGTGTGTGTGCGGCCCGCTGTGATGGC 789

RESULT 3
US-10-000-157-5
; Sequence 5, Application US/10000157
; Publication No. US20020182673A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul L.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovashnik, Melissa.
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P4(US)
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;; PRIOR FILING DATE: 2000-11-10  
;; PRIOR APPLICATION NUMBER: PCT/US00/32678  
;; PRIOR FILING DATE: 2000-12-01  
;; PRIOR APPLICATION NUMBER: PCT/US00/34956  
;; PRIOR FILING DATE: 2000-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US01/06520  
;; PRIOR FILING DATE: 2001-02-28  
;; PRIOR APPLICATION NUMBER: PCT/US01/17800  
;; PRIOR FILING DATE: 2001-06-01  
;; PRIOR APPLICATION NUMBER: PCT/US01/19692  
;; PRIOR FILING DATE: 2001-06-20  
;; PRIOR APPLICATION NUMBER: PCT/US01/21066  
;; PRIOR FILING DATE: 2001-06-29  
;; PRIOR APPLICATION NUMBER: PCT/US01/21735  
;; PRIOR FILING DATE: 2001-07-09  
;; NUMBER OF SEQ ID NOS: 39  
;; SEQ ID NO 5  
;; LENGTH: 1320  
;; TYPE: DNA  
;; ORGANISM: Homo Sapien  
US-10-000-157-5

Alignment Scores:  
Pred. No.: 4,85e-92 Length: 1320  
Score: 898.00 Matches: 159  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.68% Indels: 0  
DB: 9 Gaps: 0

US-10-037-591A-2 (1-161) x US-10-000-157-5 (1-1320)

QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22  
DB 313 CAGGTGGTTCATCTTGGCAATGTCATGGGAACCCACACCTACAGCCACTGCCCCAGC 372  
QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42  
DB 373 TGTGCCCCAGCAAGGCGAGCACCTCTGAGGAGCTGCTGAGGTGGAGCAGCTGTGCCT 432  
QY 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62  
DB 433 GTGCCTCCCTTAGAGCCTGTAGGCCCAACCCAGCAGAGTCTGTAGGGCCAGTGAA 492  
QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeu 82  
DB 493 GATGGACCCCTCAACAGCAGGGCCATCTCCCTGGAGATATGATGGACAGAGACTTG 552  
QY 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102  
DB 553 AACCGGCTCCCCAGGACCTGTACACGCGCGTGTGCCTGTGCCGCACTGCCGTCAGCCTA 612  
QY 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122  
DB 613 CAGACAGGCTCCCATATGGACCCCGGGCAACTCGGAGCTGCTTACCAACACAGACT 672  
QY 123 ValPheTyrArgProCysHisGlyGlnLysGlyThrHisLysGlyTyrCysLeuGlu 142  
DB 673 GTCTTCTACAGCGCGCCATGCCATGGCGAAGGCGACCCCAAGGGCTACTGCTGGAG 732  
QY 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161  
DB 733 CGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGCGGCCCCCGTGTATGGGC 789

## RESULT 4

US-10-063-547-155  
;; Sequence 155, Application US/10063547  
;; Publication No. US20020182638A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, Christopher J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; FILE REFERENCE: P3230R1C1  
;; CURRENT APPLICATION NUMBER: US/10/063,547  
;; CURRENT FILING DATE: 2002-05-02  
;; Prior Application removed - See File Wrapper or Palm  
;; NUMBER OF SEQ ID NOS: 170  
;; SEQ ID NO 155  
;; LENGTH: 1320  
;; TYPE: DNA  
;; ORGANISM: Homo Sapien  
US-10-063-547-155

Alignment Scores:  
Pred. No.: 4,85e-92 Length: 1320  
Score: 898.00 Matches: 159  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.68% Indels: 0  
DB: 9 Gaps: 0

US-10-037-591A-2 (1-161) x US-10-063-547-155 (1-1320)

QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22  
DB 313 CAGGTGGTTCATCTTGGCAATGTCATGGGAACCCACACCTACAGCCACTGCCCCAGC 372  
QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42  
DB 373 TGTGCCCCAGCAAGGCGAGCACCTCTGAGGAGCTGCTGAGGTGGAGCAGCTGTGCCT 432  
QY 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62  
DB 433 GTGCCTCCCTTAGAGCCTGTAGGCCCAACCCAGCAGAGTCTGTAGGGCCAGTGAA 492  
QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeu 82  
DB 493 GATGGACCCCTCAACAGCAGGGCCATCTCCCTGGAGATATGATGGACAGAGACTTG 552  
QY 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102  
DB 553 AACCGGCTCCCCAGGACCTGTACACGCGCGTGTGCCTGTGCCGCACTGCCGTCAGCCTA 612  
QY 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122  
DB 613 CAGACAGGCTCCCATATGGACCCCGGGCAACTCGGAGCTGCTTACCAACACAGACT 672  
QY 123 ValPheTyrArgProCysHisGlyGlnLysGlyThrHisLysGlyTyrCysLeuGlu 142  
DB 673 GTCTTCTACAGCGCGCCATGCCATGGCGAAGGCGACCCCAAGGGCTACTGCTGGAG 732  
QY 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161  
DB 733 CGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGCGGCCCCCGTGTATGGGC 789

## RESULT 5

US-09-747-259-5  
;; Sequence 5, Application US/09747259  
;; Publication No. US20030008815A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Genentech, Inc.  
;; APPLICANT: Chen, Jian  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul  
;; APPLICANT: Grimaldi, Christopher  
;; APPLICANT: Gurney, Austin

```

; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR FILING DATE: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 5
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-747-259-5

Alignment Scores:
Pred. No.: 4,85e-92 Length: 1320
Score: 898.00 Matches: 159
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.68% Indels: 0
DB: 9 Gaps: 0

US-10-037-591A-2 (1-161) x US-09-747-259-5 (1-1320)

QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22
Db 313 CAGGTGGTTGCATCTTGGCAATGGTCAATGGGAACCCACACCTACAGCCACTGGCCAGC 372
QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
Db 373 TGCTGCCCCAGCAAGGCGAGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCT 432
QY 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62
Db 433 GTGCCTCCCTAGAGCTGTAGGCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAA 492

; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 155
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-155

Alignment Scores:
Pred. No.: 4,85e-92 Length: 1320
Score: 898.00 Matches: 159
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.68% Indels: 0
DB: 9 Gaps: 0

US-10-037-591A-2 (1-161) x US-10-063-616-155 (1-1320)

QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22
Db 313 CAGGTGGTTGCATCTTGGCAATGGTCAATGGGAACCCACACCTACAGCCACTGGCCAGC 372
QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
Db 373 TGCTGCCCCAGCAAGGCGAGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCT 432
QY 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62
Db 433 GTGCCTCCCTAGAGCTGTAGGCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAA 492
QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu 82
Db 493 GATGGACCCCTCAACAGCAGGGCCATCTCCCTCTGGAGATATGATTTGGACAGACTTG 552

; Sequence 155, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 155
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-155

RESULT 6
US-10-063-616-155
; Sequence 155, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 155
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-155

QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu 82
Db 493 GATGGACCCCTCAACAGCAGGGCCATCTCCCTCTGGAGATATGATTTGGACAGACTTG 552
QY 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102
Db 553 AACCGGCTCCCGCAGGACCTGTACACGCGCCGCTGCTGCTGCGCCGCACTGGCTCAGCCTA 612
QY 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122
Db 613 CAGACAGGCTCCACATGGACCCCGGGGCACTCGGAGCTGCTCTACCAACACAGACT 672
QY 123 ValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142
Db 673 GTCTTCTACAGCGCGCCATGCCATGGCGAGAGGGGACCCACCAAGGGCTACTGCTGGAG 732
QY 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161
Db 733 CGCAGGCTGTACCGTGTTCCTTAGCTGTGTGTGTGGGCGCCGCTGTGATGGC 789

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 155
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-155

Alignment Scores:
Pred. No.: 4,85e-92 Length: 1320
Score: 898.00 Matches: 159
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.68% Indels: 0
DB: 9 Gaps: 0

US-10-037-591A-2 (1-161) x US-10-063-616-155 (1-1320)

QY 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22
Db 313 CAGGTGGTTGCATCTTGGCAATGGTCAATGGGAACCCACACCTACAGCCACTGGCCAGC 372
QY 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
Db 373 TGCTGCCCCAGCAAGGCGAGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCT 432
QY 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62
Db 433 GTGCCTCCCTAGAGCTGTAGGCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAA 492
QY 63 AspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu 82
Db 493 GATGGACCCCTCAACAGCAGGGCCATCTCCCTCTGGAGATATGATTTGGACAGACTTG 552
```



|                                                                           |     |                                                                 |     |
|---------------------------------------------------------------------------|-----|-----------------------------------------------------------------|-----|
| Qy                                                                        | 123 | ValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu    | 14  |
| Db                                                                        | 673 | GTCTTTCTACAGCGCGCCATGCGCATGGCGAGAAGGCGACCCACCAAGGGCTACTCGCTGGAG | 732 |
| Qy                                                                        | 143 | ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly       | 161 |
| Db                                                                        | 733 | CGCAGGCTGTACCGTGTTCCTTAGCTGTGTGTGTGGCGCCCGTGTGATGGGC            | 789 |
| RESULT 9                                                                  |     |                                                                 |     |
| US-10-063-598-155                                                         |     |                                                                 |     |
| : Sequence 155, Application US/10063598                                   |     |                                                                 |     |
| : Publication No. US20030050462A1                                         |     |                                                                 |     |
| : GENERAL INFORMATION:                                                    |     |                                                                 |     |
| : APPLICANT: Eaton,Dan L.                                                 |     |                                                                 |     |
| : APPLICANT: Filvaroff, Ellen                                             |     |                                                                 |     |
| : APPLICANT: Gerritsen, Mary E.                                           |     |                                                                 |     |
| : APPLICANT: Goddard, Audrey                                              |     |                                                                 |     |
| : APPLICANT: Godowski, Paul J.                                            |     |                                                                 |     |
| : APPLICANT: Grimaldi, Christopher J.                                     |     |                                                                 |     |
| : APPLICANT: Gurney, Austin L.                                            |     |                                                                 |     |
| : APPLICANT: Watanabe, Colin K.                                           |     |                                                                 |     |
| : APPLICANT: Wood, William I.                                             |     |                                                                 |     |
| : TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC |     |                                                                 |     |
| : FILE REFERENCE: P3230R1C1                                               |     |                                                                 |     |
| : CURRENT APPLICATION NUMBER: US/10/063,598                               |     |                                                                 |     |
| : CURRENT FILING DATE: 2002-05-03                                         |     |                                                                 |     |
| : Prior Application removed - See File Wrapper or Palm                    |     |                                                                 |     |
| : NUMBER OF SEQ ID NOS: 170                                               |     |                                                                 |     |
| : SEQ ID NO 155                                                           |     |                                                                 |     |
| : LENGTH: 1320                                                            |     |                                                                 |     |
| : TYPE: DNA                                                               |     |                                                                 |     |
| : ORGANISM: Homo Sapien                                                   |     |                                                                 |     |
| US-10-063-598-155                                                         |     |                                                                 |     |
| Alignment Scores:                                                         |     |                                                                 |     |
| Pred. No.: 4,85e-92 Length: 1320                                          |     |                                                                 |     |
| Score: 898.00 Matches: 159                                                |     |                                                                 |     |
| Percent Similarity: 100.00% Conservative: 0                               |     |                                                                 |     |
| Best Local Similarity: 100.00% Mismatches: 0                              |     |                                                                 |     |
| Query Match: 98.68% Indels: 0                                             |     |                                                                 |     |
| DB: 9 Gaps: 0                                                             |     |                                                                 |     |
| US-10-037-591A-2 (1-161) x US-10-063-598-155 (1-1320)                     |     |                                                                 |     |
| Qy                                                                        | 3   | GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer    | 22  |
| Db                                                                        | 313 | CAGTGTTGTCATCTCTGGCAATGGTCATGGGAACCCACACCTACAGGCACCTGGCCACG     | 372 |
| Qy                                                                        | 23  | CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro    | 42  |
| Db                                                                        | 373 | TGCTGCCCCAGCAAGGCGAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGGCT     | 432 |
| Qy                                                                        | 43  | ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu    | 62  |
| Db                                                                        | 433 | GTGCCTCCCTTAGAGCTGTCTAGGCCAACCGCCACCCAGAGTCCTGTAGGSCCAGTGAA     | 492 |
| Qy                                                                        | 63  | AspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu    | 82  |
| Db                                                                        | 493 | GATGGAGCCCTCAACAGCAGGGGCCATCTCCCCCTGGAGATATGAGTTGGACAGACTTG     | 552 |
| Qy                                                                        | 83  | AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu    | 102 |
| Db                                                                        | 553 | AACGGGCTCCCCAGAGACCTGTACCAAGCGCCCTTGCTGTGCCCGCAGCTGCGTCAGCCCTA  | 612 |
| Qy                                                                        | 103 | GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr    | 122 |
| Db                                                                        | 613 | CAGACAGGCTCCCCACATGGACCCCGGGGCAACTCGGAGCTGCTCTACACACACAGACT     | 672 |
| Qy                                                                        | 123 | ValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu    | 142 |
| Db                                                                        | 673 | GTCTTTCTACAGCGCGCCATGCGCATGGCGAGAAGGCGACCCACCAAGGGCTACTCGCTGGAG | 732 |

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Db 613 CAGACAGGCTCCACATAGGAGCCCGGGGCAACTCGGAGCTGCTCTACCACACAGACT 672
Qy 123 ValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142
Db 673 GTCTTCTACAGGCGCCATGCCATGGCGAGAGGCGACCCACACAGGCTACTGCTGGAG 732
Qy 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161
Db 733 CGCAGGCTGTACCGTGTCTTCTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 789

RESULT 11
US-09-908-827-5
; Sequence 5, Application US/09908827
; Publication No. US2003005442A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: PL381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/908,827
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/113,621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/130,232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131,022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/134,287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/138,387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/213,807
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/244,072
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380,138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380,142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854,208
; PRIOR FILING DATE: 2001-05-10
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; PRIOR APPLICATION NUMBER: 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 5
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-908-827-5

Alignment Scores:
Pred. No.: 4,85e-92 Length: 1320
Score: 898.00 Matches: 159
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.68% Indels: 0
Db: 9 Gaps: 0

US-10-037-591A-2 (1-161) x US-09-908-827-5 (1-1320)

Qy 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisLysProSer 22
Db 313 CAGGTGGTTGCATTCTTGGCAATGTCATGGAACCCACACCTACAGCCACTGGCCAGC 372
Qy 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
Db 373 TGCTGCCCCAGCAAGGCGCAGGACACCTCTGAGGAGCTCTGAGGTGGAGCACTGTGCCT 432
Qy 43 ValProProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAlaSerGlu 62
Db 433 GTGCTCCCTAGAGCTGCTAGGCCCCAACCCGACAGAGTCTCTGTAGGGCCACTGAA 492
Qy 63 AspGlyProLeuAsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgLeu 82
Db 493 GATGAGCCCTCAACAGCAGGCGCAATCTCCCTCGGAGATATGAGTTGACACAGACTTG 552
Qy 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102
Db 553 AACCGGCTCCCCCAGGACCTGTACCAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
Qy 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122
Db 613 CAGACAGGCTCCCATGTGACCCCGGGGCAACTCGAGAGTCTGCTTACCACACAGACT 672
Qy 123 ValPheTyrArgArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142
Db 673 GTCTTCTACAGGCGCCATGCCATGGCGAGAGGCGACCCACCAAGGGCTACTGCCCTGGAG 732
```





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Db 733 CGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGGGGCCCCGGTGTGATGGGC 789
RESULT 14
US-10-063-599-155
; Sequence 155, Application US/10063599
; Publication No. US20030078387A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,599
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 155
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-599-155

Alignment Scores:
Pred. No.: 4.85e-92 Length: 1320
Score: 898.00 Matches: 159
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.68% Indels: 0
Gaps: 9
DB:

US-10-037-591A-2 (1-161) x US-10-063-599-155 (1-1320)
Qy 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22
Db 313 CAGTGGTGTGATCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCCAGC 372
Qy 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
Db 373 TGTGCCCCAGCAAGGCGAGCACCTCTGAGGAGTGTCTGAGTGAGCACTGTGCCT 432
Qy 43 ValProProLeuGluProAlaAArgProAsnArgHisProGluSerCysArgAlaSerGlu 62
Db 433 GTGCCTCCCTTAGAGCCTGTAGGCCCAACCCGCCACCCAGAGTCTCTGAGGGCCAGTGAA 492
Qy 63 AspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu 82
Db 493 GATGAGCCCTTACACAGCAGGCGCCATCTCCCTCCCTGGAGATATGATGGACAGACTTG 552
Qy 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102
Db 553 AACCGGCTCCCGCAGGACCTGTACACGCCGCTTGCCTGTGCCGCACTGGCTCAGCCCTA 612
Qy 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122
Db 613 CAGACAGGCTCCCATATGAGCCCGGGGCAACTCGGAGCTGCTTACCAACACAGACT 672
Qy 123 ValPheTyrArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142
Db 673 GTCCTTACAGCGGCCCATGCGATGGCGAGAGGGGCCACCCACAGGGGTACTGCTGCTGGAG 732
Qy 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161
Db 733 CGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGGGGCCCCCGTGTGATGGGC 789
RESULT 15
US-10-212-912-17
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; Sequence 17, Application US/10212912
; Publication No. US20030077737A1
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE OF INVENTION: Related Diseases
; FILE REFERENCE: P3133R1C2
; CURRENT APPLICATION NUMBER: US/10/212,912
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/052,594
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/172,059
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 17
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-212-912-17

Alignment Scores:
Pred. No.: 4.85e-92 Length: 1320
Score: 898.00 Matches: 159
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.68% Indels: 0
Gaps: 9
DB:

US-10-037-591A-2 (1-161) x US-10-212-912-17 (1-1320)
Qy 3 GlnValValAlaPheLeuAlaMetValMetGlyThrHisThrTyrSerHisTrpProSer 22
Db 313 CAGTGGTGTGATCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCCAGC 372
Qy 23 CysCysProSerLysGlyGlnAspThrSerGluGluLeuLeuArgTrpSerThrValPro 42
Db 373 TGTGCCCCAGCAAGGCGAGCACCTCTGAGGAGTGTCTGAGTGAGCACTGTGCCT 432
Qy 43 ValProProLeuGluProAlaAArgProAsnArgHisProGluSerCysArgAlaSerGlu 62
Db 433 GTGCCTCCCTTAGAGCCTGTAGGCCCAACCCGCCACCCAGAGTCTCTGAGGGCCAGTGAA 492
Qy 63 AspGlyProLeuAsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeu 82
Db 493 GATGAGCCCTTACACAGCAGGCGCCATCTCCCTCCCTGGAGATATGATGGACAGACTTG 552
Qy 83 AsnArgLeuProGlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeu 102
Db 553 AACCGGCTCCCGCAGGACCTGTACACGCCGCTTGCCTGTGCCGCACTGGCTCAGCCCTA 612
Qy 103 GlnThrGlySerHisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThr 122
Db 613 CAGACAGGCTCCCATATGAGCCCGGGGCAACTCGGAGCTGCTTACCAACACAGACT 672
Qy 123 ValPheTyrArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGlu 142
Db 673 GTCCTTACAGCGGCCCATGCGATGGCGAGAGGGGCCACCCACAGGGGTACTGCTGCTGGAG 732
Qy 143 ArgArgLeuTyrArgValSerLeuAlaCysValCysValArgProArgValMetGly 161
Db 733 CGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGGGGCCCCCGTGTGATGGGC 789
```

Search completed: May 12, 2003, 02:56:36  
Job time : 102 secs

---

GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 12, 2003, 02:01:34 ; Search time 1059 Seconds  
(without alignments)  
2462.203 Million cell updates/sec

Title: US-10-037-591A-2

Perfect score: 910

Sequence: 1 MYQVAFAMVMGTHTYSHW.....ERRLYRSLVCVCRPRVMG 161

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh  
-Q/cgn2\_1/USPTO\_spool/US10037591/runat\_06052003\_123154\_22289/app\_query.fasta\_1.327  
-DB=EST -OPMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USPR=US10037591.ecgn\_1\_1.1456 @runat\_06052003\_123154\_22289 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estom:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_man:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID       | Description        |
|------------|-------|---------------|--------|----|----------|--------------------|
| 1          | 594   | 65.3          | 524    | 9  | AI430337 | AI430337 mf68b10.y |
| 2          | 493   | 54.2          | 420    | 14 | W88186   | W88186 mf68b10.r1  |
| 3          | 345   | 37.9          | 344    | 12 | BG609875 | BG609875 324181.MA |
| 4          | 337   | 37.0          | 553    | 13 | BM540145 | BM540145 hb18f07.g |
| 5          | 139   | 15.3          | 549    | 14 | BQ554452 | BQ554452 H4028C03- |
| 6          | 126.5 | 13.9          | 432    | 10 | BE108127 | BE108127 UI-R-CA0- |
| 7          | 126.5 | 13.9          | 511    | 12 | BF409208 | BF409208 UI-R-BT1- |
| 8          | 126.5 | 13.9          | 533    | 14 | BQ211497 | BQ211497 UI-R-DY1- |
| 9          | 126.5 | 13.9          | 561    | 14 | BQ209760 | BQ209760 UI-R-DZ1- |
| 10         | 126   | 13.8          | 678    | 14 | BQ604493 | BQ604493 MI-P-CP1- |
| 11         | 125.5 | 13.8          | 373    | 9  | AI867949 | AI867949 wb90b08.x |
| 12         | 125.5 | 13.8          | 405    | 9  | AI375735 | AI375735 ta64c02.x |
| 13         | 125.5 | 13.8          | 467    | 9  | AI370793 | AI370793 ta58a04.x |
| 14         | 125.5 | 13.8          | 468    | 9  | AA780147 | AA780147 af37c02.s |
| 15         | 125.5 | 13.8          | 568    | 14 | BQ574994 | BQ574994 UI-H-E21- |
| 16         | 125.5 | 13.8          | 629    | 14 | BM826445 | BM826445 K-EST0098 |
| 17         | 125.5 | 13.8          | 647    | 12 | BF476508 | BF476508 naa27b03  |
| 18         | 124.5 | 13.7          | 870    | 13 | BI413156 | BI413156 602990024 |
| 19         | 123.5 | 13.6          | 504    | 9  | AI645992 | AI645992 vw53h08.x |
| 20         | 123.5 | 13.6          | 749    | 11 | AK003506 | AK003506 Mus muscu |
| 21         | 120.5 | 13.2          | 502    | 12 | BF408277 | BF408277 UI-R-BJ2- |
| 22         | 119.5 | 13.1          | 717    | 13 | BI408737 | BI408737 602964519 |
| 23         | 119   | 13.1          | 441    | 9  | AI275406 | AI275406 ql63c10.x |
| 24         | 116.5 | 12.8          | 579    | 9  | AA763404 | AA763404 vw53h08.r |
| 25         | 115.5 | 12.7          | 590    | 12 | BF510968 | BF510968 UI-H-B14- |
| 26         | 115   | 12.6          | 396    | 9  | AA680405 | AA680405 z138h02.s |
| 27         | 114.5 | 12.6          | 369    | 13 | BI274883 | BI274883 UI-R-CW0- |
| 28         | 112.5 | 12.4          | 366    | 9  | AA960023 | AA960023 vw53h08.s |
| 29         | 110.5 | 12.1          | 718    | 13 | BI561289 | BI561289 603256441 |
| 30         | 110.5 | 12.1          | 836    | 13 | BI828970 | BI828970 603074846 |
| 31         | 109   | 12.0          | 633    | 12 | BF682066 | BF682066 602117154 |
| 32         | 108   | 11.9          | 437    | 14 | W89980   | W89980 mf39h11.r1  |
| 33         | 108   | 11.9          | 488    | 14 | W87101   | W87101 mf38e01.r1  |
| 34         | 108   | 11.9          | 497    | 9  | AA044549 | AA044549 mj12c03.r |
| 35         | 108   | 11.9          | 499    | 14 | W83241   | W83241 mf23g06.r1  |
| 36         | 108   | 11.9          | 662    | 10 | BE307772 | BE307772 601097115 |
| 37         | 107   | 11.8          | 469    | 9  | AA015563 | AA015563 mi61d10.r |
| 38         | 105.5 | 11.6          | 397    | 9  | AA443286 | AA443286 zw87h02.s |
| 39         | 105   | 11.5          | 652    | 10 | BB629840 | BB629840 BB629840  |
| 40         | 105   | 11.5          | 771    | 13 | BI733853 | BI733853 603353138 |
| 41         | 104.5 | 11.5          | 503    | 12 | BG368728 | BG368728 HVSME1002 |
| 42         | 103.5 | 11.4          | 691    | 12 | BF682781 | BF682781 602117154 |
| 43         | 102   | 11.2          | 483    | 10 | BE211563 | BE211563 so63d08.y |
| 44         | 101.5 | 11.2          | 639    | 9  | AJ457515 | AJ457515 AJ457515  |
| 45         | 100   | 11.0          | 970    | 17 | CNS042FU | AL271443 Tetraodon |

# ALIGNMENTS

RESULT 1  
AI430337  
LOCUS AI430337  
DEFINITION mf68b10.yl Soares mouse embryo NBME13.5 14.5 Mus musculus CDNA  
clone IMAGE:419419 5', mRNA sequence.  
ACCESSION AI430337  
VERSION AI430337.1 GI:4276173  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 524)  
AUTHORS Maria.M. Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

524 bp mRNA linear EST 15-MAR-2000  
14.5 Mus musculus CDNA







Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu  
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized hippocampus library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)  
Seq primer: M13 Forward  
POLYA=yes.

## FEATURES

source

Location/Qualifiers

1..432  
/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-CA0-axa-f-12-0-UI"  
/clone\_lib="UI-R-CA0"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; The UI-R-CA0 library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, medulla, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at [ratest.eng.uiowa.edu](http://ratest.eng.uiowa.edu). The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)  
TAG\_LIB=UI-R-CA0  
TAG\_TISSUE=hippocampus  
TAG\_SEQ=GATTG

BASE COUNT 86 a 112 c 133 g 101 t

ORIGIN

## Alignment Scores:

Pred. No.: 0.0155 Length: 432  
Score: 126.50 Matches: 29  
Percent Similarity: 52.22% Conservative: 18  
Best Local Similarity: 32.22% Mismatches: 38  
Query Match: 13.90% Indels: 5  
DB: 10 Gaps: 3

US-10-037-591A-2 (1-161) x BE108127 (1-432)

Qy 67 AsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeuAsnArgLeuPro 86  
Db 383 AACAGAGAGAGCGTCTCTCCCTGGGCTACAGCATCAATCAGCCCGCGCATCCG 324  
Qy 87 GlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySer 106  
Db 323 GAGACTTCCTGAGCGCGGTGCTATGTTGGTGGTGGTGAACCCCTTCACC----- 270  
Qy 107 HisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArg 126  
Db 269 ATGCAGGAGGACCGTAGCATGTCAGCGTCGACGTGTCACCGAGGTCCAGTCGCCGCGC 210  
Qy 127 ArgProCysHisGlyGluGlyThrHisLysGlyTyrCysLeuGluArgLeuTyr 146  
Db 209 CGCCTCTGT-----CCGCAACCTCCTCGCGCGGCGCTCGCGCAGCGTGTTCATG 156  
Qy 147 Arg---ValSerLeuAlaCysValCysVal 155  
Db 155 GAGACCATCGCTGTGGGTGCACCTGCATC 126

## RESULT 7

BF409208/c

LOCUS

DEFINITION

UI-R-BT1-bkn-c-11-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone

ACCESSION

BF409208

VERSION

BF409208 511 bp mRNA linear EST 28-NOV-2000  
UI-R-BT1-bkn-c-11-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone  
BF409208  
BF409208.1 GI:11397183

## KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

## REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

EST.

Norway rat.

Rattus norvegicus

1 (bases 1 to 511)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to identify it as a clone from the

normalized hippocampus library cDNA Library Preparation: M.B.

Soares Lab Clone distribution: clones will be available through

Research Genetics (www.resgen.com)

Seq primer: M13 Forward

POLYA=yes.

## FEATURES

source

Location/Qualifiers

1..511

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-BT1-bkn-c-11-0-UI"

/clone\_lib="UI-R-BT1"

/dev\_stage="adult"

/lab\_host="DH10B (Life Technologies)"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site.1: Not I; Site.2: Eco RI; The library

UI-R-BT1 is a subtracted library derived from a mixture of

the following tissues: hippocampus, thalamus, mid-brain,

medulla, corpus striatum, cerebral cortex and testis. For

a detailed description of the library from which this

clone was derived, please visit our web site at

[ratest.eng.uiowa.edu](http://ratest.eng.uiowa.edu). The subtraction has been previously

described in (Bonaldo, Lennon and Soares, Genome Research

6:791-806, 1996)

TAG\_LIB=UI-R-BT1

TAG\_TISSUE=hippocampus

TAG\_SEQ=GATTG

BASE COUNT 97 a 138 c 152 g 124 t

ORIGIN

## Alignment Scores:

Pred. No.: 0.0196 Length: 511  
Score: 126.50 Matches: 29  
Percent Similarity: 52.22% Conservative: 18  
Best Local Similarity: 32.22% Mismatches: 38  
Query Match: 13.90% Indels: 5  
DB: 12 Gaps: 3

US-10-037-591A-2 (1-161) x BF409208 (1-511)

Qy 67 AsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeuAsnArgLeuPro 86  
Db 384 AACAGAGAGAGCGTCTCTCCCTGGGCTACAGCATCAATCAGCCCGCGCATCCG 325  
Qy 87 GlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySer 106  
Db 324 GAGACTTCCTGAGCGCGGTGCTATGTTGGTGGTGGTGAACCCCTTCACC----- 271  
Qy 107 HisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArg 126





```

source
1. .561
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-DZ1-cog-i-01-0-UI"
/clone_lib="UI-R-DZ1"
/tissue_type="Chondrosarcoma"
/dev_stage="37 days"
/lab_host="DH10B (Life Technologies)"
/notes="Organ: Spine; Vector: p7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI;
UI-R-DZ1 is a normalized cDNA library containing the
following tissue(s): Swarm Rat Chondrosarcoma. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into p7T3D-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dt)18 tail. The sequence tag for this library is
CATCTCTGTA. The Rat cartilaginous tumor tissue was
provided by Dr Jeff Stevens at the University of Iowa.
TAG_LIB=UI-R-DZ1
TAG_TISSUE=cartilaginous tumor
TAG_SEQ=CATCTCTGTA"
BASE COUNT 107 a 154 c 173 g 127 t
ORIGIN

Alignment Scores:
Pred. No.: 0.0223 Length: 561
Score: 126.50 Matches: 29
Percent Similarity: 52.22% Conservative: 18
Best Local Similarity: 32.22% Mismatches: 38
Query Match: 13.90% Indels: 5
DB: 14 Gaps: 3

US-10-037-591A-2 (1-161) x B0209760 (1-561)
Qy 67 AsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeuAsnArgLeuPro 86
Db 384 AACAGAGAGAGCGCTCTCCCTGGGGCTACAGCATCAATCAGACCCAGCGCATCCG 325
Qy 87 GlnAspLeuTyrHisAlaArgCysLeuSerProHisCysValSerLeuGlnThrGlySer 106
Db 324 GAGACTTCCTGAGCGCGGGTGCTATGTTGGGTGGTGAACCCCTTACC----- 271
Qy 107 HisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArg 126
Db 270 ATGCAGGAGGACCGTAGCATGGTGGAGCGTGCAGGTTCAGCCAGCGTCCAGTGCAGCGC 211
Qy 127 ArgProCysHisGlyGluGlyThrHisLysGlyTyrCysLeuGluArgLeuTyr 146
Db 210 CGCCTCTGT-----CCGCAACCTCTCGCGCGCGCGCTGCGCCAGCGTGTGTCATG 157
Qy 147 Arg---ValSerLeuAlaCysValCysVal 155
Db 156 GAGACCATCGTGTGGGTGCACCTGCATC 127

RESULT 10
B0604493/c 678 bp mRNA linear EST 24-JUN-2002
LOCUS
DEFINITION MI-P-CPI-nzc-b-11-0-UI.s1 MI-P-CPI Sus scrofa cDNA clone
MI-P-CPI-nzc-b-11-0-UI 3', mRNA sequence.
ACCESSION B0604493
VERSION B0604493.1 GI:21551219
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 678)

```

Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
Contact: Tuggle CK  
Molecular Genetics Laboratory, Department of Animal Science  
Iowa State University  
201 Kildee Hall, Ames, IA 50011-3150, USA  
Tel: 5152944252  
Fax: 5152942401  
Email: cktuggle@iastate.edu  
Tissue Procurement: Dr. Chris Tuggle, Iowa State University  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).  
The following repetitive elements were found in this cDNA  
sequence: 243-304, >GC-rich#Low\_complexity (matched complement)  
Seq primer: M13 FORWARD  
POLYA-Yes.

Location/Qualifiers  
1. .678  
/organism="Sus scrofa"  
/strain="crossbreed"  
/db\_xref="taxon:9823"  
/clone="MI-P-CPI-nzc-b-11-0-UI"  
/clone\_lib="MI-P-CPI"  
/lab\_host="DH10B (Life Technologies)"  
/notes="Vector: p7T3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not 1; Site 2: EcoRI; The MI-P-CPI  
library is normalized library derived from the MI-P-CPI  
library, ultimately derived from uterine tissue. For a  
detailed description of the library from which this clone  
was derived, please visit our web site at  
http://pigest.genome.iastate.edu/. The procedure used to  
create this library has been previously described (Bonaldo  
, Lennon and Soares, Genome Research 6: 791-806, 1996)  
TAG\_LIB=MI-P-CPI  
TAG\_TISSUE=uterus  
TAG\_SEQ=AGTCCAATCG"

BASE COUNT 95 a 216 c 224 g 142 t 1 others  
ORIGIN

Alignment Scores:  
Pred. No.: 0.0323 Length: 678  
Score: 126.00 Matches: 34  
Percent Similarity: 44.25% Conservative: 16  
Best Local Similarity: 30.09% Mismatches: 39  
Query Match: 13.85% Indels: 24  
DB: 14 Gaps: 4

US-10-037-591A-2 (1-161) x B0604493 (1-678)  
Qy 67 AsnSerArgAlaIleSerProTyrArgTyrGluLeuAspArgAspLeuAsnArgLeuPro 86  
Db 465 AACACAGAGAGCGCTGTACCCCTGGGGCTACAGCATCAACACACCCAGCGCATCCCC 406  
Qy 87 GlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySer 106  
Db 405 GCGGACCTGCCGAGCGCGGTGCTGTCTGGGGTGTGTGAACCCCTTACC----- 352  
Qy 107 HisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArg 126  
Db 351 ATGCAGGAGGACCGCAGCATGGTGGAGCGTGCCTGTTTCAGCCAGCGTCCCGTGCAGCGC 292  
Qy 127 ArgProCysHisGlyGluGlyThrHisLysGlyTyrCysLeuGluArgLeuTyr 146  
Db 291 CGCCTCTGTCCCTGTCACCGCGGCACC-----GGGCCCTGTGCGCGCGCGGTGTCATG 238  
Qy 147 Arg---ValSerLeuAlaCysValCysVal----- 155  
Db 156 GAGACCATCGTGTGGGTGCACCTGCATC 127

```

Db 237 GAGACCATCGCGGGCTGCACCTGCATCTTCTGAGACGCCCTCCCGCGCCCCCAGCC 178
Qy 156 -----ArgProArgVal 159
Db 177 GCGAGCCAGGCGCGGGTGAAGCAGACCTCGGGTC 139

RESULT 11
AI867949/c 373 bp mRNA linear EST 17-DEC-1999
LOCUS wb90808.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2312919 3'
DEFINITION similar to contains Alu repetitive element; mRNA sequence.
ACCESSION AI867949
VERSION AI867949.1 GI:5540965
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 373)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 764 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 305.
Location/Qualifiers
source
1. 373
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2312919"
/clone_lib="NCI_CGAP_Pr28"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clones
985608-986759, 110192-1101959, and 1217928-1220615).
985608-986759, 110192-1101959, and 1217928-1220615."
Subtraction by Bento Soares and M. Fatima Bonaldo.
BASE COUNT 66 a 109 c 131 g 67 t.
ORIGIN

Alignment Scores:
Pred. No.: 0.0158 Length: 373
Score: 125.50 Matches: 30
Percent Similarity: 51.11% Conservative: 16
Best Local Similarity: 33.33% Mismatches: 39
Query Match: 13.79% Indels: 5
DB: 9 Gaps: 3

US-10-037-591A-2 (1-161) x AI867949 (1-373)

Qy 67 AsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuPro 86
Db 326 AACAGAGGAGCGCTGTCCTCCCTGGGGCTACAGCATCAACACGACGCCCGGTATCCCC 267
Qy 87 GlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySer 106

```

```

Db 266 GTGACCTCGCCGAGGACGCGTGTGTCTGGGCTGTGTGAACCCCTTCACC----- 213
Qy 107 HisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArg 126
Db 212 ATGCAGGAGGACCGCAGCATGTGTGCGGTGTTTCACGACGAGTCTCTGTGCGCCGC 153
Qy 127 ArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGluArgArgLeuTyr 146
Db 152 GCGCTCTCGCGCCACCCCGCCGACAC-----GGCCCTTGGCCGACGCGCAGTCATG 99
Qy 147 Arg---ValSerLeuAlaCysValCysVal 155
Db 98 GAGACCATCGCTGTGGGCTGCACCTGCATC 69

RESULT 12
AI375735/c 405 bp mRNA linear EST 16-FEB-1999
LOCUS t664C02.x1 Soares_total_fetus_Nb2HF8.9w Homo sapiens cDNA clone
DEFINITION IMAGE:2048834 3' similar to contains MER22.b1 TAR1 repetitive
element; mRNA sequence.
ACCESSION AI375735
VERSION AI375735
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 405)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 750 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 403.
Location/Qualifiers
source
1. 405
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2048834"
/clone_lib="Soares_total_fetus_Nb2HF8.9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site: 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTCGAGCGCGCTTAATTTTATTTTATTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 73 a 114 c 133 g 85 t
ORIGIN

Alignment Scores:
Pred. No.: 0.0177 Length: 405
Score: 125.50 Matches: 30
Percent Similarity: 51.11% Conservative: 16
Best Local Similarity: 33.33% Mismatches: 39
Query Match: 13.79% Indels: 5
DB: 9 Gaps: 3

US-10-037-591A-2 (1-161) x AI375735 (1-405)

Qy 67 AsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuPro 86
Db 367 AACAGAGGAGCGCTGTCTCCCTGGGGCTACAGCATCAACACGACGCCCGGTATCCCC 308

```

```

QY 87 GlnAspLeuTyrHisAlaArgCysProHisCysValSerLeuGlnThrGlySer 106
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 307 GTGGACCTGCCGAGCAGCGTGTCTGGCGCTGTGAACCCCTTCACCC----- 254
QY 107 HisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArg 126
    :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 253 ATGCAGGAGGACCGCAGCAGTGTGAGCGTGGCGGTGTTTCAGCCAGGTTCTCTGCGCGCG 194
QY 127 ArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGluArgGlyLeuTyr 146
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 193 CGCTCTCTCCCGCCACCGCCCGGCACAC-----GGGCTTGGCGCAGCGCGCAGTCATG 140
QY 147 Arg---ValSerLeuAlaCysValCysVal 155
    :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 139 GAGACCATCGTGTGGGTGCACCTGCATC 110

RESULT 13
LOCUS AI370793 467 bp mRNA linear EST 16-FEB-1999
DEFINITION ta58a04.xl Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:2048238 3', mRNA sequence.
ACCESSION AI370793
VERSION AI370793.1 GI:4149546
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 467)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: ccgaps-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 794 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 439.
FEATURES
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        1..467
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:2048238"
            /clone_lib="Soares_total_fetus_Nb2HF8_9w"
            /dev_stage="8-9 weeks"
            /lab_host="DH10B"
            /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer
[5'
TGTTACCAATCTGAAGTGGAGCGCGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 83 a 135 c 144 g 105 t
ORIGIN
Alignment Scores:
Pred. No.: 0.0216 Length: 467
Score: 125.50 Matches: 30
Percent Similarity: 51.11% Conservativeness: 16
Best Local Similarity: 33.33% Mismatches: 39
Query Match: 13.79% Indels: 5
DB: 9 Gaps: 3

US-10-037-591A-2 (1-161) x AI370793 (1-467)
QY 67 AsnSerArgAlaIleSerProTrpArgTyrGluLeuAspArgAspLeuAsnArgLeuPro 86

```

```

Db 369 ACAAGAGAGCGCTGTCTCCTGGGCTACAGCATCAACCCACCGCGTATCCCC 310
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 87 GlnAspLeuTyrHisAlaArgCysLeuCysProHisCysValSerLeuGlnThrGlySer 106
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 309 GTGGACCTGCCGAGCAGCGTGTCTGGCGCTGTGAACCCCTTCACCC----- 256
QY 107 HisMetAspProArgGlyAsnSerGluLeuLeuTyrHisAsnGlnThrValPheTyrArg 126
    :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 255 ATGCAGGAGGACCGCAGCAGTGTGAGCGTGGCGGTGTTTCAGCCAGGTTCTCTGCGCGCG 196
QY 127 ArgProCysHisGlyGluLysGlyThrHisLysGlyTyrCysLeuGluArgGlyLeuTyr 146
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 195 CGCTCTCTCCCGCCACCGCCCGGCACAC-----GGGCTTGGCGCAGCGCGCAGTCATG 142
QY 147 Arg---ValSerLeuAlaCysValCysVal 155
    :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: ||||| :::: |||||
Db 141 GAGACCATCGTGTGGGTGCACCTGCATC 112

RESULT 14
LOCUS AA780147 468 bp mRNA linear EST 05-FEB-1999
DEFINITION af37c02.sl Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:1033826 3', mRNA sequence.
ACCESSION AA780147
VERSION AA780147.1 GI:2839478
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 468)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
JOURNAL Contact: Wilson RK
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 392.
FEATURES
    source
        1..468
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:1033826"
            /clone_lib="Soares_total_fetus_Nb2HF8_9w"
            /dev_stage="8-9 weeks"
            /lab_host="DH10B"
            /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 82 a 135 c 147 g 104 t
ORIGIN
Alignment Scores:
Pred. No.: 0.0216 Length: 468
Score: 125.50 Matches: 30
Percent Similarity: 51.11% Conservativeness: 16

```



GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003. Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 12, 2003, 01:06:09 ; Search time 1066 Seconds  
(without alignments)  
9784.140 Million cell updates/sec

Title: US-10-037-591A-1

Perfect score: 644

Sequence: 1 ctcaagtcactccctaaaaa.....ggcccggtgtagggcgtag 644

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estnu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: gb\_gss.\*  
18: em\_gss\_hum.\*  
19: em\_gss\_inv.\*  
20: em\_gss\_pln.\*  
21: em\_gss\_vrt.\*  
22: em\_gss\_fun.\*  
23: em\_gss\_mam.\*  
24: em\_gss\_mus.\*  
25: em\_gss\_other.\*  
26: em\_gss\_pro.\*  
27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 296.4 | 46.0        | 524    | 9  | AI430337    |
| 2          | 249.6 | 38.8        | 420    | 14 | W88186      |
| 3          | 229   | 35.6        | 553    | 13 | BM540145    |
| 4          | 145.4 | 22.6        | 344    | 12 | BG609875    |
| 5          | 96.6  | 15.0        | 480    | 13 | BM124559    |
| 6          | 96.6  | 15.0        | 549    | 14 | BQ554452    |

|   |    |      |     |      |    |          |                     |
|---|----|------|-----|------|----|----------|---------------------|
| C | 7  | 47.4 | 7.4 | 925  | 17 | CNS0091P | AL053013 Drosophila |
| C | 8  | 47   | 7.3 | 997  | 17 | CNS006DN | AL065132 Drosophila |
| C | 9  | 43.8 | 6.8 | 868  | 12 | BG821981 | BG821981 602726077  |
| C | 10 | 43.2 | 6.7 | 925  | 17 | CNS0091P | AL053013 Drosophila |
| C | 11 | 43   | 6.7 | 568  | 14 | BQ574994 | BQ574994 UI-H-E21-  |
| C | 12 | 42.8 | 6.6 | 440  | 14 | BQ779177 | BQ779177 946117505  |
| C | 13 | 42.4 | 6.6 | 839  | 17 | CNS004NB | AL054280 Drosophila |
| C | 14 | 42.2 | 6.6 | 460  | 10 | BE357122 | BE357122 DGL_146_B  |
| C | 15 | 42.2 | 6.6 | 486  | 9  | AI388531 | AI388531 GH19472.5  |
| C | 16 | 42.2 | 6.6 | 586  | 10 | BE357121 | BE357121 DGL_146_B  |
| C | 17 | 42.2 | 6.6 | 588  | 13 | BM055698 | BM055698 1885h04.X  |
| C | 18 | 42.2 | 6.6 | 533  | 13 | BM330143 | BM330143 PIC_47_F   |
| C | 19 | 42.2 | 6.6 | 652  | 10 | BE362682 | BE362682 DGL_88_H0  |
| C | 20 | 41.6 | 6.5 | 441  | 9  | AI064196 | AI064196 GH04480.5  |
| C | 21 | 41.4 | 6.4 | 373  | 9  | AI867949 | AI867949 WB90808.X  |
| C | 22 | 41.4 | 6.4 | 396  | 9  | AA680405 | AA680405 Z138h02.S  |
| C | 23 | 41.4 | 6.4 | 405  | 9  | AI375735 | AI375735 t864C02.X  |
| C | 24 | 41.4 | 6.4 | 590  | 12 | BF510968 | BF510968 UI-H-B14-  |
| C | 25 | 41.4 | 6.4 | 629  | 14 | BM826445 | BM826445 K-EST0098  |
| C | 26 | 41.2 | 6.4 | 463  | 13 | BM381881 | BM381881 MEST541-D  |
| C | 27 | 41.2 | 6.4 | 488  | 9  | AI854942 | AI854942 605094E01  |
| C | 28 | 41.2 | 6.4 | 527  | 10 | AW787570 | AW787570 945011B07  |
| C | 29 | 41.2 | 6.4 | 540  | 10 | AW927918 | AW927918 945011B07  |
| C | 30 | 41.2 | 6.4 | 556  | 10 | AW787571 | AW787571 945011B07  |
| C | 31 | 41.2 | 6.4 | 567  | 10 | BE129743 | BE129743 946003H07  |
| C | 32 | 41.2 | 6.4 | 567  | 14 | BQ280219 | BQ280219 1091036B1  |
| C | 33 | 41.2 | 6.4 | 583  | 9  | AI833725 | AI833725 605094E01  |
| C | 34 | 41.2 | 6.4 | 584  | 14 | BQ279494 | BQ279494 1091036B1  |
| C | 35 | 41.2 | 6.4 | 586  | 10 | BE511474 | BE511474 946061B04  |
| C | 36 | 41.2 | 6.4 | 609  | 13 | BM381419 | BM381419 MEST534-E  |
| C | 37 | 41.2 | 6.4 | 615  | 10 | AW424676 | AW424676 707058E02  |
| C | 38 | 41   | 6.4 | 483  | 9  | AI388053 | AI388053 GH18791.5  |
| C | 39 | 40.8 | 6.3 | 1063 | 17 | CNS07A2Y | ALA36064 T3 end of  |
| C | 40 | 40.6 | 6.3 | 425  | 13 | BI396114 | BI396114 949044E02  |
| C | 41 | 40.6 | 6.3 | 441  | 13 | BM382130 | BM382130 MEST545-A  |
| C | 42 | 40.6 | 6.3 | 468  | 12 | BF150243 | BF150243 UY83602.Y  |
| C | 43 | 40.6 | 6.3 | 497  | 13 | BI388823 | BI388823 949046B01  |
| C | 44 | 40.6 | 6.3 | 553  | 9  | AI323984 | AI323984 mb22a01.X  |
| C | 45 | 40.6 | 6.3 | 602  | 13 | BM053185 | BM053185 id66d06.X  |

#### ALIGNMENTS

AI430337 524 bp mRNA linear EST 15-MAR-2000  
mf68b10.y1 Soares mouse embryo NMEL13.5 14.5 Mus musculus CDNA  
clone IMAGE:419419 5', mRNA sequence.

AI430337  
AI430337.1 GI:4276173

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

This read is a RESEQUENCE of a previously sequenced mouse clone

This read has been verified (found to hit its original self in the correct orientation)

MGI:253971

Seq primer: -40RP from Gibco

High quality sequence stop: 476

POLYA-No.

Location/Qualifiers

#### FEATURES

source

1. 524  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:419419"  
/clone\_lib="Soares mouse embryo NDM13.5 14.5"  
/sex="unknown"  
/tissue\_type="embryo"  
/dev\_stage="13.5-14.5dpc total fetus"  
/lab\_host="DH10B"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; lstr strand cDNA was primed with a Not I - oligo (dT) primer [5' TGTACCAATCTGAAGTGGAGCGCGGCGGAAATTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."  
100 a 177 c 150 g 97 t

#### BASE COUNT

Query Match 46.0%; Score 296.4; DB 9; Length 524;

Best Local Similarity 84.5%; Pred. No. 6.2e-61;

Matches 333; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 251 CTCCTGAGAGCTGCTGAGTGGAGCAGTGCCTGTGCTCCCTAGAGCCTGTAGGCC 310  
Db 11 CCCGAGAGGCTGCTGAAGTGGAGCTGTCATCTGTGTCCTCCCGCAGAGCCTCTGAGCCA 70  
QY 311 CAACCCGCCACAGAGTCTCTAGGGCCAGTGAAGATGGAGCCCTCAACAGCAGGGCCAT 370  
Db 71 CACCCACACAGCAATCTTCAGGCGCAGCAGGATGGCCCTTCACAGCAGGGCCAT 130  
QY 371 CTCCTCTGGAGATATGATGTTGGACAGAGACTTGAACCGGCTCCCCAGGACCTGTATCCA 430  
Db 131 CTCCTCTGGAGCTATGATGTTGGACAGGACTTGAATCGGCTCCCCAGGACCTGTATCCA 190  
QY 431 CGCCCGTTCCTGTCGCCGCACTGCTGCTAGCCTACAGACAGGCTCCACATGGACCCCG 490  
Db 191 CGCTCGATGCTGTGCCACACTGCTGCTAGCCTACAGACAGGCTCCACATGGACCCCGCT 250  
QY 491 GGGCAACTCGGAGTCTCTTACCAACACAGCAGTCTTCTACCGGCGGCGCATGCCATGG 550  
Db 251 GGGCAACTCGTCCCACTTTACCAACACAGCAGGCTTCTTACCGGCGGCGCATGCCATGG 310  
QY 551 CGAAGAGGCGACCAAGAGGCTACTGCTGGAGCGCAGGCTGTACCGTGTCTTCTTACG 610  
Db 311 CGAAGAGGCTACCATCGCGCTACTGCTGGAGCGCAGGCTGTACCGAGTCTCTCTTGGC 370  
QY 611 TTGTGTGTGTGGGCGGCGGCTGTGTATGGGCTAG 644  
Db 371 TTGTGTGTGTGGGCGGCGGCTGTGTATGGGCTAG 404

#### RESULT 2

W88186

LOCUS

DEFINITION

W88186

ACCESSION

W88186.1

VERSION

KEYWORDS

W88186 420 bp mRNA linear EST 12-SEP-1996  
m68b10.r1 Soares mouse embryo NDM13.5 14.5 Mus musculus cDNA  
clone IMAGE:419419 5', mRNA sequence.  
W88186  
W88186.1 GI:1542472  
EST.

#### SOURCE

ORGANISM

house mouse..

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

#### REFERENCE

AUTHORS

1 (bases 1 to 420)  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lannon,G., Soares,B., Wilson,R. and  
Waterston,R.

#### TITLE

JOURNAL

COMMENT

The WashU-HMI Mouse EST Project

Unpublished (1996)

On Sep 12, 1996 this sequence version replaced gi:1402263.

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

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This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:253971

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 408.

#### FEATURES

source

Location/Qualifiers

1. 420  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_lib="Soares mouse embryo NDM13.5 14.5"  
/sex="unknown"  
/tissue\_type="embryo"  
/dev\_stage="13.5-14.5dpc total fetus"  
/lab\_host="DH10B"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; lstr strand cDNA was primed with a Not I - oligo (dT) primer [5' TGTACCAATCTGAAGTGGAGCGCGGCGGAAATTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."  
82 a 140 c 118 g 80 t

#### BASE COUNT

ORIGIN

Query Match 38.8%; Score 249.6; DB 14; Length 420;  
Best Local Similarity 80.1%; Pred. No. 1.1e-49;  
Matches 330; Conservative 0; Mismatches 79; Indels 3; Gaps 3;  
QY 233 CAGCAAGGGCAGGACACCTCTGAGGAGCTCTGAGTGGAGCAGCTGTCCTGTGCTCC 292  
Db 3 CGGCACAGGGCGCACAAAGCCCGGAGAGTGGCTGAAGTGGAGCTCTGCTATATCC 62  
QY 293 CCTAGAGCTCTAGGCGCCACCGCCAGAGTCTCTGAGGCGGCGGCGGCGGCGGCGG 352  
Db 63 CCCAGAGCTCTGAGCGCCACCGCCAGAGATCTCTGAGGCGGCGGCGGCGGCGGCGG 121  
QY 353 CCTCAACAGCAGGCGCATCTCCCTGGAGATATGAGTGGACAGAGACTTGAACCGGCT 412  
Db 122 TCTCAACAGCAGGCGCATCTCTCTTGGAGTATGAGTGGACAGGAGTGAATCGGGT 181  
QY 413 CCCCCAGGACCTGTACCAACCGCCCTGCTGTGCGCCGCACTGCGCTACAGACAGG 472  
Db 182 CCCCCAGGAGCTGTACCAACCGCTGCTGTGCGCCGCTGCTGCGCCGCTGCTGCTGCT 241  
QY 473 CTCCCATGATGACCCCGGCGCACTCGGAGCTGCTTACCAACAGCAGAGCTGCTCTTA 532

|                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                              |                             |
|-----------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|-----------------------------|
| Ddb                   | 242                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | CTCCACATGGACCGCTGGGCAACTCCGTCCTCCACTTTACACACACAGCAGCGTCTTCTA | 301                         |
| Qy                    | 533                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | COGGGGCCATGCCATGGCGAGAGGGCACCCACCAAGGCTACTCCTGGAGCGCAGGCT    | 592                         |
| Ddb                   | 302                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | CCGGGGCCATG-CATGGCGAGAGGTACCCATCGCGCTACTGCTTGGAGCGCAGG-T     | 359                         |
| Qy                    | 593                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | GTACCGTGTTCCTTACCTTGTGTGTGTGTGGGCCCCGTGTGATGGGCTAG           | 644                         |
| Ddb                   | 360                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | CTACCGAGTCTCTGGCTGTGTGTGTGTGGGCCCCGGGTCTAGGCTTAG             | 411                         |
| RESULT 3              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                              |                             |
| BM540145              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                              |                             |
| LOCUS                 | BM540145                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 553 bp                                                       | mRNA linear EST 20-FEB-2002 |
| DEFINITION            | hb18f07.g1 Canis cDNAs from testes cells Canis familiaris cDNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                              |                             |
| ACCESSION             | BM540145                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                              |                             |
| VERSION               | BM540145.1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | GI:18822687                                                  |                             |
| KEYWORDS              | EST.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                              |                             |
| SOURCE                | dog.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                              |                             |
| ORGANISM              | Canis familiaris                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                              |                             |
| REFERENCE             | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                              |                             |
| AUTHORS               | 1 (bases 1 to 553)<br>O'Shaughnessy,A.L., McCombie,W.R., Baker,J.P., Baliya,V., Cunniss<br>D., Dedhia,N.N., de la Bastide,M., Katzenberger,F., King,L.,<br>Kirchoff,K.A., Miller,B., Muller,S., Nascimento,L.U., Palmer,L.,<br>Santos,L., Shah,R.S., Spiegelel,L.A., Zutavern,T., Preston,R. and<br>Hannon,G.J.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                              |                             |
| TITLE                 | Expressed sequence tags from Canis familiaris (dog) (2002)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                              |                             |
| JOURNAL               | Unpublished (2002)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                              |                             |
| COMMENT               | Contact: W. Richard McCombie<br>Lita Annenberg Hazen Genome Sequencing Center<br>Cold Spring Harbor Laboratory<br>PO Box 100, Cold Spring Harbor, NY 11724, USA<br>Tel: 516 367 8884<br>Fax: 516 367 8874<br>Email: mcombie@cshl.org<br>Plate: hb18 row: f column: 07<br>Seq primer: -21M13UnivRev<br>High quality sequence stop: 553.<br>Location/Qualifiers<br>1..553<br>/organism="Canis familiaris"<br>/db_xref="taxon:9615"<br>/clone="hb18f07"<br>/clone_lib="Canis cDNAs from testes cells"<br>/tissue_type="testes"<br>/note="Vector: Lambda zap II; The library was produced by<br>Greg Hannon and Raymond Preston (Cold Spring Harbor<br>Laboratory). This library is oligo(dT) primed using<br>Stratagene zap cDNA synthesis kit. It was made from dog<br>testes. Please contact Greg Hannon (hannon@cshl.org) with<br>any library related inquiries."<br>138 a 171 c 143 g 101 t |                                                              |                             |
| BASE COUNT            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                              |                             |
| ORIGIN                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                              |                             |
| Query Match           | 35.6%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Score 229;                                                   | DB 13; Length 553;          |
| Best Local Similarity | 74.6%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Pred. No. le-44;                                             |                             |
| Matches               | 341; Conservative                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 0; Mismatches                                                | 85; Indels 31; Gaps 3;      |
| Qy                    | 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | GTCACTCCCTAAAGACAGTGGAAATAAATTTCAATAAACAAACAGGCTTGCTGAAAA    | 65                          |
| Db                    | 104                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | GTGGCCCTCACATCAGGTGCTGGAAATAAATTTGAATAAACAAACAGGTTGCTGAAA    | 163                         |
| Qy                    | 66                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | TAAATCAGGACTCCTACCTGCTCCAGTCAGCTGGCTTCCACGAGGCGCTGTCAAGTCAGT | 125                         |
| Db                    | 164                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | TAAACACGAGCACCGGAGCTGCTCCAGTCAGCTGCCCC                       | 217                         |
| Qy                    | 126                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | CCCCCATTTGATGATGATGTGTCAGTGCCTCCAGCATGATACAGGTGGTTCATTTGGCA  | 185                         |
| Db                    | 218                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | GTAGCAC-CGTGGGTGGCGCAGCATCAGCATGAATCAGGTGATGCTGTTCTTGTA      | 276                         |



|                                                  |                                                                        |                                                                   |
|--------------------------------------------------|------------------------------------------------------------------------|-------------------------------------------------------------------|
| Best Local Similarity 99.8%; Pred. No. 1.4e-123; |                                                                        |                                                                   |
| Matches 504;                                     | Conservative 0;                                                        | Mismatches 0; Indels 1; Gaps                                      |
| QY                                               | 140                                                                    | TCAGTGTGCAGTGGCCAGCATGTACAGGTGGTTCATTTCTTGGCAATGTGTCATGGGAAC 199  |
| Db                                               | 1                                                                      | TCAGTGTGCAGTG - CCAGCATGTACAGGTGGTTCATTTCTTGGCAATGTGTCATGGGAAC 59 |
| QY                                               | 200                                                                    | CCACACTACAGCCACTGGCCAGCTGCTGCCCCAGCAAAAGGCGAGGACACTCTGTGAGGA 259  |
| Db                                               | 60                                                                     | CCACACTACAGCCACTGGCCAGCTGCTGCCCCAGCAAAAGGCGAGGACACTCTGTGAGGA 119  |
| QY                                               | 260                                                                    | GCTGCTGAGTGGAGCACTGTGCTGTGCTTCCCTAGAGCCTGTCTAGGCCCCAACCGCCA 319   |
| Db                                               | 120                                                                    | GCTGCTGAGTGGAGCACTGTGCTGTGCTTCCCTAGAGCCTGTCTAGGCCCCAACCGCCA 179   |
| QY                                               | 320                                                                    | CCACAGTCTCTTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCTCCCCCTG 379   |
| Db                                               | 180                                                                    | CCACAGTCTCTTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCTCCCCCTG 239   |
| QY                                               | 380                                                                    | GAGATAGTGTGGACAGAGACTTGAACGGGCTCCCCAGAGCACTGTACACGCCCGCTTG 439    |
| Db                                               | 240                                                                    | GAGATAGTGTGGACAGAGACTTGAACGGGCTCCCCAGAGCACTGTACACGCCCGCTTG 299    |
| QY                                               | 440                                                                    | CTGTGCCCGCACTGGTCAGCCTCAGACAGGCTCCACATGGAGCCGCCCGGGCAACTC 499     |
| Db                                               | 300                                                                    | CTGTGCCCGCACTGGTCAGCCTCAGACAGGCTCCACATGGAGCCGCCCGGGCAACTC 359     |
| QY                                               | 500                                                                    | GGAGCTGCTTACCACAACAGACTGTCTTCTACGGGGGCCATGCCATGGCGAAGGG 559       |
| Db                                               | 360                                                                    | GGAGCTGCTTACCACAACAGACTGTCTTCTACGGGGGCCATGCCATGGCGAAGGG 419       |
| QY                                               | 560                                                                    | CACCCACAAGGGCTACTGCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTG 619      |
| Db                                               | 420                                                                    | CACCCACAAGGGCTACTGCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTG 479      |
| QY                                               | 620                                                                    | TGTGCGGCCCGCTGTGATGGCTAG 644                                      |
| Db                                               | 480                                                                    | TGTGCGGCCCGCTGTGATGGCTAG 504                                      |
| RESULT 5                                         |                                                                        |                                                                   |
| ABR02393                                         |                                                                        |                                                                   |
| ID                                               | ABR02393 standard; DNA; 504 BP.                                        |                                                                   |
| XX                                               | AC ABR02393;                                                           |                                                                   |
| XX                                               | AC ABR02393;                                                           |                                                                   |
| DT                                               | 26-FEB-2002 (first entry)                                              |                                                                   |
| XX                                               | Human interleukin 174 (IL-174)-encoding DNA.                           |                                                                   |
| DE                                               | Human; interleukin 174; IL-174; cytokine; Th2 response;                |                                                                   |
| XX                                               | innate immune response; inflammation; gut cell growth;                 |                                                                   |
| KW                                               | extramedullary haematopoiesis; antibody response; granuloma formation  |                                                                   |
| KW                                               | autoimmune condition; multiple sclerosis; systemic lupus erythematosus |                                                                   |
| KW                                               | rheumatoid arthritis; diabetes; psoriasis; infectious agent.           |                                                                   |
| KW                                               | inflammatory condition; Crohn's disease; ulcerative colitis;           |                                                                   |
| KW                                               | pancreatitis; hepatitis; allergy; Th2-mediated condition;              |                                                                   |
| KW                                               | systemic anaphylactic response; skin hypersensitivity response;        |                                                                   |
| KW                                               | dermatitis; asthma; fibrosis; eosinophilic gastritis; immunomodulator  |                                                                   |
| KW                                               | antiinflammatory; antiarthritic; antidiabetic; antifungal;             |                                                                   |
| KW                                               | dermatological; neuroprotective; antiallergic; agonist; antagonist; d  |                                                                   |
| XX                                               | Homo sapiens.                                                          |                                                                   |
| OS                                               | Homo sapiens.                                                          |                                                                   |
| XX                                               | Key Location/Qualifiers                                                |                                                                   |
| PH                                               | 19...504                                                               |                                                                   |
| FT                                               | CDS                                                                    |                                                                   |
| FT                                               | /*tag= a                                                               |                                                                   |
| FT                                               | /product= "Human IL-174"                                               |                                                                   |
| FT                                               | 19..66                                                                 |                                                                   |
| FT                                               | /*tag= b                                                               |                                                                   |
| FT                                               | 67..501                                                                |                                                                   |
| FT                                               | /*tag= c                                                               |                                                                   |
| FT                                               | /product= "Mature human IL-174"                                        |                                                                   |
| FT                                               | mat_peptide                                                            |                                                                   |
| FT                                               | sig_peptide                                                            |                                                                   |

FT Modified-site /note= "protein kinase C phosphorylation site"  
FT Modified-site 43  
FT Modified-site /note= "phosphorylation site"  
FT Modified-site 45..47  
FT Modified-site /note= "calcium phosphorylation site"  
FT Modified-site 53  
FT Modified-site /note= "phosphorylation site"  
FT Modified-site 53..56  
FT Modified-site /note= "cAMP protein kinase phosphorylation site"  
FT Modified-site 56  
FT Modified-site /note= "phosphorylation site"  
FT Modified-site 95  
FT Modified-site /note= "phosphorylation site"  
FT Modified-site 95..98  
FT Modified-site /note= "cAMP protein kinase phosphorylation site"  
FT Modified-site 95..102  
FT Modified-site /note= "tyrosine kinase site"  
FT Modified-site 98  
FT Modified-site /note= "phosphorylation site"  
FT Modified-site 104..107  
FT Modified-site /note= "N-glycosylation site"  
FT Modified-site 115..119  
FT Modified-site /note= "myristoylation site"  
FT Modified-site 118..122  
FT Modified-site /note= "myristoylation site"  
FT Modified-site 119..121  
FT Modified-site /note= "protein kinase C phosphorylation site"  
FT Modified-site 131  
FT Modified-site /note= "phosphorylation site"  
XX W0200042188-A2.  
XX 20-JUL-2000.  
XX 10-JAN-2000; 2000WO-US000006.  
XX 11-JAN-1999; 99US-0228822.  
XX (SCHE ) SCHERING CORP.  
XX Gorman DM, Bazan JF, Kasteleins RA;  
XX WPI: 2000-466130/40.  
XX N-PSDB; RAA53986.  
XX New isolated polynucleotide encoding a mammalian Interleukin-17 like  
XX protein used to identify genes for homologous proteins -  
XX Claim 11; Page 16; 11lpp; English.  
XX The present sequence represents an interleukin-174 (IL-174) polypeptide.  
XX The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a  
XX member of a new group of interleukins, IL-170 polypeptides. The members  
XX comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170  
XX protein can be used to treat abnormal proliferation e.g. cancer  
XX or degenerative conditions. Antibodies can be used in diagnostic  
XX methods to detect over production of IL-170 protein in cells or body  
XX fluids.  
XX Sequence 161 AA;  
SQ Query Match 100.0%; Score 910; DB 21; Length 161;  
Best Local Similarity 100.0%; Pred. No. 4.1e-86;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 MYQVAFAMVWGTHYSHWPCCKGDTSEELLRWSTVPVPLEPARNRHPESCRA 60  
Db 1 MYQVAFAMVWGTHYSHWPCCKGDTSEELLRWSTVPVPLEPARNRHPESCRA 60  
Oy 61 SEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQGTGSHMDPRGNSSELLYHN 120  
Db 61 SEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQGTGSHMDPRGNSSELLYHN 120

Oy 121 QTVFRRPCHGKGTGKGYCLERRLYRSLACVCPVRVMG 161  
Db 121 QTVFRRPCHGKGTGKGYCLERRLYRSLACVCPVRVMG 161  
RESULT 2  
AAB07692  
ID AAB07692 standard; Protein; 161 AA.  
XX AC AAB07692;  
XX 07-NOV-2000 (first entry)  
XX A human interleukin-174 polypeptide.  
XX Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;  
XX IL-174; IL-176; IL-177; cell proliferation; cancer.  
XX Homo sapiens.  
XX OS  
XX Key Location/Qualifiers  
XX Peptide 1..16 /note= "signal peptide"  
XX Modified-site 15..17 /note= "calcium phosphorylation site"  
XX Modified-site 16..18 /note= "calcium phosphorylation site"  
XX Modified-site 12..16 /note= "myristoylation site"  
XX Protein 17..161 /note= "mature protein"  
XX Modified-site 21 /note= "phosphorylation site"  
XX Modified-site 21..24 /note= "cAMP protein kinase phosphorylation site"  
XX Modified-site 23 /note= "phosphorylation site"  
XX Modified-site 41..43 /note= "protein kinase C phosphorylation site"  
XX Modified-site 43 /note= "phosphorylation site"  
XX Modified-site 45..47 /note= "calcium phosphorylation site"  
XX Modified-site 53 /note= "phosphorylation site"  
XX Modified-site 53..56 /note= "cAMP protein kinase phosphorylation site"  
XX Modified-site 56 /note= "phosphorylation site"  
XX Modified-site 95 /note= "phosphorylation site"  
XX Modified-site 95..98 /note= "cAMP protein kinase phosphorylation site"  
XX Modified-site 95..102 /note= "tyrosine kinase site"  
XX Modified-site 98 /note= "phosphorylation site"  
XX Modified-site 104..107 /note= "N-glycosylation site"  
XX Modified-site 115..119 /note= "myristoylation site"  
XX Modified-site 118..122 /note= "myristoylation site"  
XX Modified-site 119..121 /note= "protein kinase C phosphorylation site"  
XX Modified-site 131 /note= "phosphorylation site"  
XX W0200042187-A1.  
XX 20-JUL-2000.  
XX 10-JAN-2000; 2000WO-US000005.  
PF

XX PR 11-JAN-1999; 99US-0229402.  
 XX PA (SCHE ) SCHERING CORP.  
 XX PI Gorman DM, Bazan JF, Kastelein RA;  
 XX DR WPI; 2000-476060/41.  
 XX DR N-PSDB; AAA59158.  
 XX PT New DNA sequence encoding a mammalian homolog of CTLA-8, designated  
 XX PT interleukin-171 (IL-171), useful for recombinant production of IL-171  
 XX PT which can be used for treating conditions associated with abnormal  
 XX PT physiology or development.  
 XX PS Disclosure; Page 19; ilipp; English.  
 XX CC The present sequence represents an interleukin (IL)-174 polypeptide.  
 XX CC It is a mammalian homologue of the cytokine designated CTLA-8 (also  
 XX CC referred to as IL-17). The specification also describes homologues  
 XX CC IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA  
 XX CC sequence encoding IL-171 is useful for identifying genes, mRNA and  
 XX CC cDNA molecules which code for related or homologous proteins. The  
 XX CC IL-171 protein, antibodies against IL-171, and compounds which have  
 XX CC binding affinity to IL-171 are useful in treatment of conditions  
 XX CC associated with abnormal physiology or development, including abnormal  
 XX CC proliferation, e.g. cancerous conditions, or degenerative conditions.  
 XX CC The IL-171 protein can be used in kits and assay methods for identifying  
 XX CC compounds that selectively bind to IL-171.  
 XX SQ Sequence 161 AA;  
 Query Match 100.0%; Score 910; DB 21; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 4.le-86;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MYQVAFAMVGMTHYSHWPCSCPSKGQDTSELLRWSTVPVPPLEPARNRHPESCA 60  
 DB 1 MYQVAFAMVGMTHYSHWPCSCPSKGQDTSELLRWSTVPVPPLEPARNRHPESCA 60  
 QY 61 SEDGPLNSRAISPWRYELDRDLNRLPDQLYHARCLCPHCVSLQTGSHMDPRGNSSELYHN 120  
 DB 61 SEDGPLNSRAISPWRYELDRDLNRLPDQLYHARCLCPHCVSLQTGSHMDPRGNSSELYHN 120  
 QY 121 QTVFYRRPCHGKGTGKGYCLERRLRYSLACVCRVRVMG 161  
 DB 121 QTVFYRRPCHGKGTGKGYCLERRLRYSLACVCRVRVMG 161  
 RESULT 3  
 AAEL18120  
 ID AAE18120 standard; Protein; 161 AA.  
 XX AC AAE18120;  
 XX DT 07-MAY-2002 (first entry)  
 XX DE Human Interleukin-17 like (IL-17L) protein.  
 XX KW Human; interleukin-17 like; IL-17L; immune system dysfunction; diabetes;  
 XX KW cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus;  
 XX KW inflammatory bowel disease; neuronal dysfunction; transplant rejection;  
 XX KW autoimmune disorder; lung; skin; kidney; bone; eye; vascular system;  
 XX KW infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;  
 XX KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;  
 XX KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;  
 XX KW epilepsy; atherosclerosis; heart failure; angiodysplasia; endometriosis;  
 XX KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;  
 XX KW cancer.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers

Peptide 1..16  
 /label= Signal\_peptide  
 Protein 17..161  
 /label= Mature\_IL\_17L\_protein  
 WO200208285-A2.  
 31-JAN-2002.  
 21-JUN-2001; 2001WO-US19861.  
 22-JUN-2000; 2000US-213125P.  
 02-FEB-2001; 2001US-266159P.  
 16-MAR-2001; 2001US-0810384.  
 (AMGE-) AMGEN INC.  
 Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HO, Jing S;  
 WPI; 2002-155217/20.  
 N-PSDB; AAD28771.  
 Nucleic acid molecules encoding Interleukin 17 (IL-17) - like  
 polypeptides useful in the treatment, prevention and diagnosis of  
 diseases e.g. cancer  
 Claim 13; Fig 1; 242pp; English.  
 The invention relates to nucleic acid molecules encoding Interleukin 17  
 (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels  
 of IL-17 protein in an animal. The IL-17 protein is useful for treating,  
 preventing or ameliorating a disease, such as immune system dysfunction  
 (rheumatoid arthritis, osteoarthritis, diabetes, inflammatory bowel  
 autoimmune multiple sclerosis, lupus, diabetes, inflammatory bowel  
 disease, transplant rejection, graft vs. host disease); infections (HIV,  
 hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,  
 sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung  
 (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin  
 (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone  
 (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy  
 atherosclerosis, heart failure, angiodysplasia); tumours, cancers (lymphoma  
 leukaemia); reproductive (infertility, miscarriage, endometriosis), eye  
 (blindness), retinal neuropathy) and treatment of diseases involving  
 inflammation. The present sequence is human Interleukin-17 like (IL-17L)  
 protein.  
 Query Match 100.0%; Score 910; DB 23; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 4.le-86;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MYQVAFAMVGMTHYSHWPCSCPSKGQDTSELLRWSTVPVPPLEPARNRHPESCA 60  
 DB 1 MYQVAFAMVGMTHYSHWPCSCPSKGQDTSELLRWSTVPVPPLEPARNRHPESCA 60  
 QY 61 SEDGPLNSRAISPWRYELDRDLNRLPDQLYHARCLCPHCVSLQTGSHMDPRGNSSELYHN 120  
 DB 61 SEDGPLNSRAISPWRYELDRDLNRLPDQLYHARCLCPHCVSLQTGSHMDPRGNSSELYHN 120  
 QY 121 QTVFYRRPCHGKGTGKGYCLERRLRYSLACVCRVRVMG 161  
 DB 121 QTVFYRRPCHGKGTGKGYCLERRLRYSLACVCRVRVMG 161  
 RESULT 4  
 ID AAM52691  
 ID AAM52691 standard; Protein; 161 AA.  
 XX AC AAM52691;  
 XX DT 26-FEB-2002 (first entry)



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US-10-037-591A-2 (1-161) x AAA59158 (1-504)

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ID ABA02393
XX ABA02393 standard; DNA; 504 BP.
XX AC ABA02393;
XX DT 26-FEB-2002 (first entry)
XX DE Human interleukin 174 (IL-174)-encoding DNA.
XX KW Human; interleukin 174; IL-174; cytokine; Th2 response;
KW innate immune response; inflammation; gut cell growth;
KW extramedullary haematopoiesis; antibody response; granuloma formation;
KW autoimmune condition; multiple sclerosis; systemic lupus erythematosus;
KW rheumatoid arthritis; diabetes; psoriasis; infectious agent;
KW inflammatory condition; Crohn's disease; ulcerative colitis;
KW pancreatitis; hepatitis; allergy; Th2-mediated condition;
KW systemic anaphylactic response; skin hypersensitivity response;
KW dermatitis; asthma; fibrosis; eosinophilic gastritis; immunomodulator;
KW antiinflammatory; antiarthritic; antidiabetic; antifungal;
KW dermatological; neuroprotective; antiallergic; agonist; antagonist; ds.
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XX WO200179288-A2.
XX
XX 25-OCT-2001.
XX
XX 17-APR-2001; 2001WO-US12493.
XX
XX 18-APR-2000; 2000US-198488P.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Hurst SD, Zurawski SM, Rennick DM;
XX
XX WPI; 2002-034343/04.
XX
XX P-PSDB; AAM52691.
XX
XX Administering an interleukin 174 agonist or antagonist to a mammal
XX regulates various immune and inflammatory responses and is useful to
XX treat for example autoimmune diseases, allergies or response to an
XX infection
XX
XX Disclosure; Page 26-27; 29pp; English.
XX
XX The invention relates to methods of directing an immune response in a
XX mammal by the administration of an agonist or antagonist of the cytokine
XX interleukin 174 (IL-174). Administration of an IL-174 agonist directs the
XX immune response towards a Th2 response, stimulates an innate immune
XX response, augments the inflammatory response from epithelial or
XX fibroblast cells, induces gut cell growth, promotes extramedullary
XX haematopoiesis, or augments an antibody response in serum and faecal
XX material, while administration of an IL-174 antagonist directs the immune
XX response away from a Th2 type response, and prevents inflammation or
XX granuloma formation. IL-174 agonists may be used to treat autoimmune
XX conditions (particularly multiple sclerosis, systemic lupus
XX erythematosus, rheumatoid arthritis, diabetes or psoriasis), a response
XX to an infectious agent, or inflammatory conditions such as Crohn's
XX disease, ulcerative colitis, pancreatitis, or hepatitis. IL-174
XX antagonists may be used to treat inflammatory, allergic or Th2-mediated
XX conditions (e.g., systemic anaphylactic response, skin hypersensitivity
XX response, dermatitis, asthma, fibrosis, or eosinophilic gastritis). The
XX present sequence represents DNA encoding human IL-174.
XX
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Db 79 CCCAGCTGCTGCCCGCAGCAAAAGGCGAGACACCTCTGAGGAGCTGCTGAGGTGGAGCACT 138
Oy 41 ValProValProLeuGluProAlaArgProAsnArgHisProGluSerCysArgAla 60
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1320)  
AUTHORS Fong, S., Goddard, A., Godowski, P. J., Grimaldi, C. J., Gurney, A. L.,  
Hillan, K. J., Tumas, D., Watanabe, C. K., Wood, W. I., and Zhang, Z.  
TITLE Compositions and methods for the treatment of immune related  
diseases  
JOURNAL Patent: WO 0140465-A 17 07-JUN-2001;  
Genentech, Inc. (US)  
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VERSION AX180768.1 GI:15132618  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1320)  
AUTHORS Chen, J., Filvaroff, E., Fong, S., Goddard, A., Godowski, P. J.,  
Grimaldi, C. J., Gurney, A. L., Li, H., Hillan, K. J., Tumas, D., van  
Lookeren, M., Vandlen, R. L., Watanabe, C. K., Williams, P. M., Wood, W. I.,  
and Yansura, D. G.

TITLE Il-17 and il-17r homologous polypeptides and therapeutic uses  
thereof  
JOURNAL Patent: WO 0146420-A 5 28-JUN-2001;  
Genentech, Inc. (US)  
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Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 165 CAGTGGTTCATCTTGGCAATGGTCTATGGGAACCCACACCTACAGCCACTGCCCCAGC 224  
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ACCESSION AF305200  
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KEYWORDS Homo sapiens.  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1335)  
AUTHORS Lee, J., Ho, W.-H., Maruoka, M., Corpuz, R. T., Baldwin, D. T.,  
Foster, J. S., Goddard, A. D., Yansura, D. G., Vandlen, R. L., Wood, W. I.,  
and Gurney, A. L.  
TITLE IL-17E, a novel proinflammatory ligand for the IL-17 receptor  
homolog IL-17Rhl  
JOURNAL J. Biol. Chem. 276 (2), 1660-1664 (2001)  
MEDLINE 21125711  
PUBMED 11058597  
REFERENCE 2 (bases 1 to 1335)  
AUTHORS Lee, J., Ho, W.-H., Maruoka, M., Corpuz, R. T., Baldwin, D., Foster, J. S.,  
Goddard, A. D., Yansura, D. G., Vandlen, R. L., Wood, W. I. and Gurney, A. L.  
TITLE Direct Submission  
JOURNAL Submitted (12-SEP-2000) Molecular Biology, Genentech, 1 DNA Way,

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